STIC Search Report
Biotech-Chem Library

STIC Database Tracking Number: 123592

TO: Gerald G Leffers
Location: REM/2A69/2C70
Art Unit: 1636
Thursday, June 03, 2004

Case Serial Number: 09/769699

From: Alex Waclawiw
Location: Biotech-Chem Library
Rem 1A71
Phone: 272-2534

Alexandra.waclawiw@uspto.gov

Search Notes

From: Leffers, Gerald
Sent: Wednesday, June 02, 2004 2:59 PM
To: STIC-Biotech/ChemLib; Yucel, Irem
Subject: RE: 09/769,699

Can anyone give me a status update for this search? This is an After-Final case that has a fairly tight deadline on it. It would be very useful to be able to allow the claims if they are in fact free of any of the more recently issued patents and/or pending applications. Thank you for your help. Gerry Leffers

Gerald G. Leffers Jr., PhD
Primary Examiner, Art Unit 1636
Remsen Building, Room 02A69
(571) 272-0772

-----Original Message-----
From: Fredman, Jeffrey
Sent: Thursday, May 20, 2004 9:39 AM
To: STIC-Biotech/ChemLib
Cc: Leffers, Gerald
Subject: FW: 09/769,699

PLEASE RUSH.

I Approve.

Jeff Fredman

-----Original Message-----
From: Leffers, Gerald
Sent: Thursday, May 20, 2004 8:01 AM
To: Fredman, Jeffrey
Subject: 09/769,699

Hi Jeff, please approve a RUSH updated search of issued and pending files for SEQ ID NO: 2 of this application (~ 1,200 amino acid residues). This is an After-Final that may well be allowable. As always, thank you for your help. Gerry

Gerald G. Leffers Jr., PhD
Primary Examiner, Art Unit 1636
Remsen Building, Room 02A69
(571) 272-0772

Point of Contact:
Alexandra Waclawiw
Technical Info. Specialist
GM1 6A02 Tel: 308-4491

Searcher:_____
Phone:_____
Location:_____
Date Picked Up:_____ 6-3-04
Date Completed:_____ 6-3-04
Searcher Prep/Review:_____ 7
Clerical:_____
Online time:_____ 7

TYPE OF SEARCH:
NA Sequences:_____
AA Sequences:_____ ①
Structures:_____
Bibliographic:_____
Litigation:_____
Full text:_____
Patent Family:_____
Other:_____

VENDOR/COST (where applic.)
STN:_____
DIALOG:_____
Questel/Orbit:_____
DRLink:_____
Lexis/Nexis:_____
Sequence Sys.:_____
WWW/Internet:_____
Other (specify): computer

OM protein - protein search, using sw model

```
                GenCore version 5.1.6
           Copyright (c) 1993 - 2004 Compugen Ltd.
```

Run on: June 3, 2004, 07:04:28 ; Search time 23 Seconds
                                      (without alignments)
                                      2700.263 Million cell updates/sec

Title: US-09-769-699-2
Perfect score: 6294
Sequence: 1 MENTQKTVTVPTGPLGYVYA.........DELFDLSGIPIKHGNITMEM 1203

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 100 summaries

Database : Issued_Patents_AA:*
         1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
         2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
         3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
         4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
         5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
         6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                         SUMMARIES

Result No.	Score	% Query Match	DB	Length	ID	Description
1	3054	48.5	4	1452	US-09-127-227-2	Sequence 2, Appli
2	183	2.9	3	35	US-08-807-332B-9	Sequence 9, Appli
3	183	2.9	3	35	US-09-338-976-9	Sequence 9, Appli
4	131	2.1	4	757	US-09-413-814-84	Sequence 84, Appl
5	123	2.0	4	1074	US-09-071-035-358	Sequence 358, App
6	123	2.0	4	1074	US-09-071-035-394	Sequence 394, App
7	122	1.9	4	1096	US-09-134-000C-5764	Sequence 5764, Ap
8	118.5	1.9	4	370	US-09-252-991A-16913	Sequence 16913, A
9	117	1.9	4	855	US-09-489-039A-12681	Sequence 12681, A
10	111	1.8	4	4630	US-09-091-609-2	Sequence 2, Appli
11	111	1.8	5	5215	US-09-105-537-2	Sequence 2, Appli
12	110	1.7	4	790	US-09-543-681A-6059	Sequence 6059, Ap
13	106.5	1.7	2	3567	US-07-642-734C-4	Sequence 4, Appli
14	106.5	1.7	3	3567	US-08-439-009A-4	Sequence 4, Appli
15	106	1.7	4	774	US-07-731-157A-7	Sequence 7, Appli
16	106	1.7	2	774	US-08-541-780-7	Sequence 7, Appli
17	105.5	1.7	4	1095	US-08-107-532A-3855	Sequence 3855, Ap
18	105	1.7	1	774	US-08-633-760-46	Sequence 46, Appl
19	105	1.7	4	774	US-08-633-760-48	Sequence 48, Appl
20	104.5	1.7	4	635	US-08-931-608A-5	Sequence 5, Appli
21	104.5	1.7	4	635	US-09-851-847-5	Sequence 5, Appli
22	104.5	1.7	4	774	US-08-019-870-5	Sequence 5, Appli
23	104.5	1.7	4	1471	US-08-811-519-1	Sequence 5, Appli
24	103	1.6	1	774	US-08-019-870-3	Sequence 3, Appli
25	103	1.6	4	774	US-08-633-760-44	Sequence 44, Appl
26	103	1.6	4	3472	US-09-408-020-4	Sequence 4, Appli
27	102	1.6	1	729	US-08-070-165F-6	Sequence 6, Appli
28	102	1.6	2	729	US-08-885-418-6	Sequence 6, Appli
29	102	1.6	1	774	US-07-747-901A-3	Sequence 3, Appli
30	102	1.6	1	774	US-07-935-312-3	Sequence 3, Appli
31	102	1.6	1	774	US-08-633-760-50	Sequence 50, Appl
32	101.5	1.6	1	773	US-08-019-870-1	Sequence 1, Appli
33	101.5	1.6	1	773	US-08-019-870-6	Sequence 6, Appli
34	101.5	1.6	1	774	US-08-019-870-8	Sequence 8, Appli
35	101.5	1.6	1	774	US-08-019-870-11	Sequence 11, Appl
36	101	1.6	1	774	US-08-633-760-52	Sequence 52, Appl
37	101	1.6	4	995	US-09-657-031A-1	Sequence 1, Appli
38	101	1.6	4	1024	US-09-562-737-48	Sequence 48, Appl
39	101	1.6	4	1466	US-09-262-537-20	Sequence 20, Appl
40	101	1.6	3	7257	US-09-335-409-5	Sequence 5, Appli
41	101	1.6	4	7257	US-09-568-102-5	Sequence 5, Appli
42	101	1.6	4	7257	US-09-567-969-5	Sequence 5, Appli
43	101	1.6	4	7257	US-09-568-480-5	Sequence 5, Appli
44	101	1.6	4	7257	US-09-568-486-5	Sequence 5, Appli
45	101	1.6	4	7257	US-09-568-472-5	Sequence 5, Appli
46	101	1.6	4	7257	US-09-567-899-5	Sequence 5, Appli
47	100.5	1.6	5	1321	US-08-261-822A-3	Sequence 3, Appli
48	100.5	1.6	6	1321	PCT-US95-07744A-3	Sequence 3, Appli
49	100.5	1.6	6	2616	5206163-3	Patent No. 5206163-3
50	100	1.6	4	1381	US-09-808-701A-25	Sequence 25, Appl
51	99.5	1.6	4	600	US-09-252-991A-29817	Sequence 29817, A
52	99	1.6	4	915	US-08-328-322-5	Sequence 5, Appli
53	98.5	1.6	5	801	US-09-351-150A-25	Sequence 25, Appl
54	98.5	1.6	4	910	US-09-134-000C-4288	Sequence 4288, Ap
55	98.5	1.6	3	2152	US-09-036-987A-3	Sequence 3, Appli
56	98.5	1.6	3	2152	US-09-370-700-3	Sequence 3, Appli
57	98.5	1.6	4	2152	US-09-603-207-3	Sequence 3, Appli
58	98	1.6	4	551	US-09-252-991A-24209	Sequence 24209, A
59	98	1.6	2	821	US-08-451-822A-13	Sequence 13, Appl
60	98	1.6	4	821	US-08-323-430-13	Sequence 13, Appl
61	97.5	1.5	4	660	US-09-252-991A-19282	Sequence 19282, A
62	97.5	1.5	1	769	US-08-471-570-8	Sequence 8, Appli
63	97.5	1.5	4	1024	US-09-562-737-50	Sequence 50, Appl
64	97.5	1.5	4	2680	US-09-489-039A-7973	Sequence 7973, Ap
65	97	1.5	1	537	US-08-173-508-2	Sequence 2, Appli
66	97	1.5	2	537	US-08-265-310-2	Sequence 2, Appli
67	97	1.5	2	537	US-08-951-762-2	Sequence 2, Appli
68	97	1.5	4	1469	US-09-262-537-58	Sequence 58, Appl
69	96.5	1.5	4	522	US-09-543-681A-5830	Sequence 5830, Ap
70	96.5	1.5	4	987	US-09-543-681A-7785	Sequence 7785, Ap
71	96	1.5	1	774	US-08-314-309A-21	Sequence 21, Appl
72	95.5	1.5	2	3170	US-07-642-734C-5	Sequence 5, Appli
73	95.5	1.5	3	3170	US-08-439-009A-5	Sequence 5, Appli
74	94.5	1.5	4	500	US-09-071-035-396	Sequence 396, App
75	94.5	1.5	4	817	US-09-489-039A-10407	Sequence 10407, A
76	94.5	1.5	4	1073	US-09-180-245-2	Sequence 2, Appli
77	94.5	1.5	3	6095	US-09-144-085-2	Sequence 2, Appli
78	94	1.5	4	550	US-09-328-352-5508	Sequence 5508, Ap
79	94	1.5	1	655	US-07-736-178C-2	Sequence 2, Appli
80	94	1.5	2	2910	US-08-466-033-183	Sequence 183, App
81	94	1.5	2	2910	US-08-444-733-183	Sequence 183, App
82	94	1.5	2	2910	US-08-464-134-183	Sequence 183, App
83	94	1.5	2	2910	US-08-461-361-183	Sequence 183, App
84	94	1.5	2	2910	US-08-485-910-183	Sequence 183, App
85	94	1.5	5	2910	PCT-US95-06266-157	Sequence 157, App
86	93.5	1.5	4	389	US-09-596-824-2	Sequence 2, Appli
87	93.5	1.5	4	544	US-09-198-452A-153	Sequence 153, App
88	93.5	1.5	3	685	US-08-947-965-74	Sequence 74, Appl
89	93.5	1.5	3	1536	US-09-413-814-10	Sequence 10, Appl
90	93.5	1.5	2	3038	US-08-450-332-2	Sequence 2, Appli
91	93.5	1.5	2	3038	US-08-637-640-2	Sequence 2, Appli
92	93.5	1.5	2	3241	US-09-004-406C-2	Sequence 2, Appli
93	93	1.5	3	1113	US-09-041-786-1	Sequence 1, Appli
94	93	1.5	3	1113	US-09-629-616-3	Sequence 3, Appli
95	93	1.5	4	1177	US-08-754-490-10	Sequence 10, Appl
96	93	1.5	4	1177	US-08-922-505A-10	Sequence 10, Appl
97	93	1.5	3	1177	US-08-922-505A-12	Sequence 12, Appl
98	93	1.5	3	1177	US-09-260-952A-10	Sequence 10, Appl
99	93	1.5	3	1177	US-09-260-952A-10	Sequence 10, Appl
100	93	1.5	3	1177	US-09-260-952A-12	Sequence 12, Appl
```

ALIGNMENTS

RESULT 1

US-09-127-227-2

; Sequence 2, Application US/09127227
; Patent No. 6399354
; GENERAL INFORMATION:
;  APPLICANT: David M. Knipe
;  APPLICANT: Travis J. Taylor
;  APPLICANT: Elizabeth McNamee
;  TITLE OF INVENTION: Replication-Competent Virus Expressing A
;  TITLE OF INVENTION: Fusion Protein
;  FILE REFERENCE: HU98-05
;  CURRENT APPLICATION NUMBER: US/09/127,227
;  CURRENT FILING DATE: 1998-07-31
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
;  LENGTH: 1452
;  TYPE: PRT
;  ORGANISM: herpesvirus
US-09-127-227-2

Query Match       48.5%;   Score 3054;  DB 4;  Length 1452;
Best Local Similarity  49.8%;   Pred. No. 2.7e-304;
Matches  609;  Conservative 200;  Mismatches 366;  Indels  48;  Gaps  17;

Qy    1 MENTQKTVT---VPTGPLGIVY--ACRVEDLDLEEISFLAARSTDSDLALLPLMRNLTVE  55
          |||  ||    ||||||:||  :|  |:|: ||:|:| |||:|::|| :||||||:|| ||
Db    1 METKPKTATTIKVPPGPLGYVYARACPSEGIEL--LALLSARSGDADVAVAPLVVGLTVE  58

Qy   56 KTFTSSLAVVSGGARTGLAGAGITLKLTTSHFYPSVFVFHGGKHVLPSSAAPNLTRACNA 115
          |||:|||| |||||||:||||||||||||||:|||: :|||| :|||: ||||||||:|||
Db   56 KTFTSSLAVVSGGARTGLAGAGITLKLTTSHFYPSVFVFHGGKHVLPSSAAPNLTRACNA 115

Db   59 SGFEANVAVVVGSRTTGLGGTAVSLKLTPSHYSSSVYVFHGGRHLDPSTQAPNLTRLCER 118

Qy  116 ARERFGFSRCQGPPVDGAVETTGAEICTRLGLEPENTILYLVVTALFKEAVFMCNVFLHY 175
          ||:: :||:| ||: :::|: ||| :|   :||||: | :|:| ||:: :||:|::||:
Db  119 ARRHFGFSDYTPRPGDLKHETTGEALCERLGLDPDRALLYLVVTEGFKEAVCINNTFLHL 178

Qy  176 GGLDIVHINHGDVIRIPLFPVQLFMPDVNRLVPDPNTHHRSIGEGFVYPTPFYNTGLCH 235
          |||| :|:| ||:||::||:||||||:|:| |::: |::||||||||| |:|||||||
Db  179 GGSDKVTIGGAEVHRIPVYPLQLFMPDFSRVIAEPFNANHRSIGENTYPLPFFNRPLNR 238

Qy  236 LIHDCVIAPMAVALRVRNVTAVARGAAHLAFDENHEGAVLPPDITVTYFQSSSSGTTTAR 295
          |:|: :|||:||| :||:|:|||: :|:|||||||||| :||:|:|||||::: :|:
Db  239 LLFEAVVGPAAVALRCRNVDAVARAAAHLAFDENHEGAALPADITFTAFEASQG--KTPR 296

Qy  296 GARRNDVNSTSKPSPSGGFERRLASIMAADTALHAEVIFNTGIYEETPTDIKEWPMFIGM 355
          |  ::|:|  ||: ::||:|:||||: :||||||  ::| : :: : |||| ||:
Db  297 GGR-----DGGGKGPAGGFEQRLASVMAGDAALALESIVSMAVFDEPPTDISAWPLCEGQ 351

Qy  356 EGTLPLRLNALGSYTARVAGVIGAMVFSPNSALYLTEVEDSGMTEAKDGGPGPSFNRFYQF 415
          || |:: |: ||| ||::| | |||||::: : |:   :|| ||| ||::|  :||:
Db  352 DTAAARANAVGAYLARAAGLVGAMVFSTNSALHLTEVDDAGPADPKDHSK-PSFYRFFLV 410

Qy  416 AGPHLAANPQTDRDGHVL------SGQSTGSSNTEFSVDYLALICGFGAPLLARLLFYL 468
          |||:|||:| ||:|  |      ||:||||::  | ::::: |:|||||::|:||:||
Db  411 PGTHVAANPQVDREGHVVPGFEGRPTAPLVGGTQ-EFAGEHIAMLCGFSPAILAKMLFYL 469

Qy  469 ERCDAGAFTGGHG-DALKVTGTFPDSEIPCSLCEKHTRPVCAHTTVHRLRQRMPRPGQAT 527
          |||| :|||||  :|||::| ||||::: |||:|  |   || | ||: :||:|:|:|||
Db  470 ERCDGGVIVGRQEMDVFRYVADSNQTDVPCNLCTFDTRHACVHTTLMRLRARHPKFASAA 529

Qy  528 RQPIGVFGTMNSQYSDCDPLGNYAPYLILRKPGDTEAAKATMQDTYRATLERLFIDLEQ 587
          ||||| |||:| ::|||:|||||||:|::|||| : |||:|||||||| || |::|| :|
Db  530 RGAIGVFGTMNSMYSDCDVLGNYAAFSALKR-ADGSETARTIMQETYRAATERVMAELET 588

Qy  588 ERLLDRGAPCSSEGLSSVIVDHPFPFRRILDTLRARIEQTTTQFMKVLVETRDYKIREGLS 647
          |||||| :|:| ||::|| :|  :: |::  :: |:||||  ::|: |:|| | |::| | 
Db  589 LQYVDQAVPTAMGRLETIITNREALHTVNNVRQVVDREVEQLMRNLVEGRNFKFRDGLG 648

Qy  648 EATHSMALTFDPYSGAFCPITNFLVKRTHLAVVQDLALSQCHCVFYGQQVEGRNFRNQFQ 707
          || ||| ||||| :: :| ||| ||| | |||:|| |||||||||| ::|||||| |||
Db  649 EANHAMSLTLDPYACGPCPLLQLLGRRSNLAVVQDLALSQCHGVFAGQSVEGRNFRNQFQ 708

Qy  708 PVLRRRFVDLFNGGFISTRSITVTLSEG-PVSAPNPTLGQDAPAGRTFDGDLARVSVEVI 766
          ||||| :||  |||| ::| | |  |:| |:|||   | : | | ::::| :| || :
Db  709 PVLRRRVMDMFNNGFLSAKTLTVALSEGAAICAPSLTAGQTAPAESSFEGDVARVTLGPP 768

Qy  767 RDIRVKNRVVFSGNCTNLSEAARARLVGLASAYORQEKRVDMLHGALGFLLKQFHGLLFP 826
          :::||| |:| ||:: |::::|  || :| |||:|||:|||||| ::|:|:|||  |: |
Db  769 KELRVKSRVLFAGASANASEAAKARVASLQSAYQKPDKRVDILLGPLGFLLKQFHAAIFP 828

Qy  827 RGMPPNSKSPNPQWFWTLLQRNQMPADKLTHEEITTIAAVKRFTEEYAAINFINLPPTCI 886
          ||| |||  |||| |||||||||:|||| ::|:||||||:|| ::|::|:||||||
Db  829 NGKPPGSNQPNPQWFWTALQRNQLPARLLSREDIETIAPIKKFSLDYGAINFINLAPNNV 888

Qy  887 GELAQFYMANLILKYCDHSQYLINTLTSIITGARRPRDPSSVLHWIRKDVTSAADIETQA 946
          |||||||:|||:|:|||:|||::| |:: :||||||||||:|| |:||:|  ::|:|
Db  889 SELAMYYMANQILRYCDHSTYFINVTLTAIIAGSRPPSVQAAAAW---SAQGGAGLEAGA 945

Qy  947 KALLEKTENLPELWTTAFTSTHLVRAAMNQRPMVVLGISISKYHGAAGNNRVFQAGNWSG 1006
          ::||:|||| |:||  || |:|||:|| :||||:||| ||||| |||:| || ||| |
Db  946 RALMDAVDAHPGAWTSMFASCNLLRPVMAARPMVVLGLSISKYYGMAGNDRVFQAGNWAS 1005

Qy 1007 LNGGKNVCPLFTFDRTRRFIIACPRGGFICPVTGPSSGNRETTLSDQVRGIIVSGGAMVQ 1066
          |||| ||||| ||||:||: | |||||| ||:||||||:| |:||||:||:|| |||| |
Db 1006 LMGGKNACPLLIFDRTRKFVLACPRAGFVCAASNLGGGAHESSLCEQLRGIISEGGAAVA 1065

Qy 1067 LAIYATVRAVGARAQHMAFDDWLSLTDDEFLARDLEELHDQIIQTLETPWTVEGAL--- 1123
          |: :: :| |    ||:  |  :|   :|:|| |  |:| |::|:| | | :|:| 
Db 1066 SSVFVATVKSLGPRTQQLQIEDWLALLEDEYLSEMMELTARALERGNGEWSTDAALEVA 1125

Qy 1124 -EAVKILDEKTTAGDGETPNLAFNFD--SCEPSHDTTSNVLNISGSNVSGGSTVPGLKRP 1180
           :|| |:|: : |  |:|||| |:| :||| ||| | |:|: || : ||:| |||||
Db 1126 HEAEAIVSQLGNAGE------VFNFGDFGCE-----DDNATPFGGPGAPGPAFAGRKRA 1173

Qy 1181 PEDDELFDLSGIPIKHGNITMEM 1203
          || :|||| ||:|::| | |:
Db 1174 FHGDDPFG-EGPPDKKGDLTLDM 1195

RESULT 2

US-08-807-332B-9

; Sequence 9, Application US/08807332B
; Patent No. 5959074
; GENERAL INFORMATION:
;  APPLICANT: Dreyfus, David H.
;  APPLICANT: Gelfand, Erwin W.
;  TITLE OF INVENTION: PRODUCTS AND PROCESSES FOR REGULATION OF
;  TITLE OF INVENTION: GENE RECOMBINATION
;  NUMBER OF SEQUENCES: 32
;  CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Sheridan Ross
;   STREET: 1700 Lincoln St., Suite 3500
;   CITY: Denver
;   STATE: CO
;   COUNTRY: U.S.A.
;   ZIP: 80203
;  COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;  CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/807,332B
;   FILING DATE: 28-FEB-1997
;   CLASSIFICATION: 435
;  ATTORNEY/AGENT INFORMATION:
;   NAME: Kovarik, Joseph E.
;   REGISTRATION NUMBER: 33,005
;   REFERENCE/DOCKET NUMBER: 2879-39
;   TELECOMMUNICATION INFORMATION:

; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
US-08-807-332B-9

Query Match     2.9%;  Score 183;  DB 2;  Length 35;
Best Local Similarity 100.0%;  Pred. No. 1.6e-11;  Indels 0;
Matches  35;  Conservative  0;  Mismatches  0;  Gaps  0;

Qy   545 DPLGNYAPYLILRKPGDQTEAAKATMQDTYRATLE 579
           |||||||||||||||||||||||||||||||||||
Db     1 DPLGNYAPYLILRKPGDQTEAAKATMQDTYRATLE 35

RESULT 3
US-09-338-876-9
; Sequence 9, Application US/09338876
; Patent No. 6187584
; GENERAL INFORMATION:
; APPLICANT: Dreyfus, David H.
; APPLICANT: Gelfand, Erwin W.
; TITLE OF INVENTION: PRODUCTS AND PROCESSES FOR REGULATION OF
; TITLE OF INVENTION: GENE RECOMBINATION
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross
; STREET: 1700 Lincoln St., Suite 3500
; CITY: Denver
; STATE: CO
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/338,876
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/807,332
; FILING DATE: 28-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Kovarik, Joseph E.
; REGISTRATION NUMBER: 33,005
; REFERENCE/DOCKET NUMBER: 2879-39
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303/863-9700
; TELEFAX: 303/863-0223
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
US-09-338-876-9

Query Match     2.9%;  Score 183;  DB 3;  Length 35;
Best Local Similarity 100.0%;  Pred. No. 1.6e-11;  Indels 0;
Matches  35;  Conservative  0;  Mismatches  0;  Gaps  0;

Qy   545 DPLGNYAPYLILRKPGDQTEAAKATMQDTYRATLE 579
           |||||||||||||||||||||||||||||||||||
Db     1 DPLGNYAPYLILRKPGDQTEAAKATMQDTYRATLE 35

RESULT 4
US-09-413-814-84
; Sequence 84, Application US/09413814
; Patent No. 6225064
; GENERAL INFORMATION:
; APPLICANT: Gesellschaft fuer Biotechnologische Forschung mbH
; APPLICANT: Bristol-Myers Squibb, Co.
; APPLICANT: Beyer, Stefan
; APPLICANT: Bloecker, Helmut
; APPLICANT: Brandt, Petra
; APPLICANT: Cino, Paul M
; APPLICANT: Dougherty, Brian A
; APPLICANT: Goldberg, Steven L
; APPLICANT: Hofle, Gerhard
; APPLICANT: Mueller, Joachim
; APPLICANT: Reichenbach, Hans
; TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or
; TITLE OF INVENTION: heteropolyketide compounds
; FILE REFERENCE: PCT/US 99/23535
; CURRENT APPLICATION NUMBER: US/09/413,814
; CURRENT FILING DATE: 1999-10-07
; EARLIER APPLICATION NUMBER: DE 198 46 493.2
; EARLIER FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
; LENGTH: 757
; TYPE: PRT
; ORGANISM: Sorangium cellulosum
US-09-413-814-84

Query Match     2.1%;  Score 131;  DB 3;  Length 757;
Best Local Similarity 21.1%;  Pred. No. 0.0012;
Matches 146;  Conservative  84;  Mismatches 251;  Indels 212;  Gaps 37;

Qy    54 VRKTFTSSLAVVSGART----TGLAGAGITLKLTTSHFYPSVFVFHGGKHVLPSSAAPNL 109
             ||  || |                 ||| ||
Db   129 LERTLPRVASIVADARAEAALTSSAVAGIVAS---------------------LPASAAA-- 167

Qy   110 TRACNAARERFGFSRCCGPVDGAVETTGAEICTRLGLEPENTILYLVVTALFKEAVFMC 169
            || |                                  |||
Db   168 -----AALQRLRWIATDGPS-PGPIEGPGA---------ALRPESV------------- 198

Qy   170 NVFLHY------GGLDIVHINHGDVIRIPLFPVQLFMPDVNRLVPDPFNTHHRSIGEGFVY 224
             |  |            |||      | |      |                  ||
Db   199 -AFLQYTSGSTGEPKGVMLTHGNL----LHNSRLIAHGFDLTSPDPV---------GVIW 244

Qy   225 PTPFYNTGLC---------HLIHDCVIAPMAVALR---VRNVTAV--ARGAAHLAFD- 267
              | |  ||          |                          |   |
Db   245 LPPYHDMGLIGGILQALYRRIRVALMSPLSFLQRPMRWLRAVSALGASVSGGPNFAYDLC 304

Qy   268 ---ENHEGAVLPPDITYTYFQSSSSGTTTARGARRNDVNSTSKPSPSGGFERRLASIMA 323
                  ||       |    ::   |        ||          :::
Db   305 VRKSSEERAALD------LRSWEVAFTGAEPVRADTLDRFARAFAVSGFRRE--AFYP 355

Qy   324 ADTALHAEVIFNTGIYEETPTDIKEWPMFIGMEGTLPRLNALGSVTARVAGVIGAMVF- 381
             |    |           |                      |   |  |
Db   356 CYGLAEATLIVSGGARAEAPV----------LARLAPEVELGRAVASAAE--GARVFVG 403

Qy   382 ----SPNSALYLTEVEDSGMTEAKDGGPGPSFNRFYQFAGPHLA---ANPQTDRDGHV 432
                  |   |  |           :    | ||:       :  ::
Db   404 SGRALDPRA---VAIVDPAG---NELGPG-EIGEIW-VSGPSVAVGYWGRPE------- 447

Qy   433 LSSQSTGSSNTEFSVDYLALICGFGAPLIARLLFYLERCDAGAFTGGHGDALKVTGT- 490
             |   | |       |       |  ||  |
Db   448 ----------ETEATFGATLAGSAAPR-----YLRTGDLGFLRGGE---LFVVGRSK 486

Qy   491 ------FDSEIPCSLCBKH--TRPVC--AHTTVHRLRQRM------PRFGQATRQ 529
              :: |                :           :
Db   487 DLIILRGRNHFPQDIEKTVESSHRAVRPGCSAAFSVEHEGBERLAVVCEVDPRVAADPRE 546

Qy   530 PIGVFGTMNSQYSDCDPLGNYAPYLILRKPGDQTEAAKATMQDTYRATLERLFIDLEQER 589

```
Db   212  ---NIDYRVIGNQLVLTP--------------------------NSNSKSGTLTLKKSAGTGTP-VAYKK  251

Qy   466  FYLERCDAGAFTGGHGDALKYVTGTFDSEIPCSLCEKHTRPVCAHTTVHRLRQRMPRFGQ  525
               :||     |||:||    : :     |                  ||:||
Db   252  AGLQTVMAGALDKPNTYAIKINVETKGS-LKIKKIDKBSGDIVPETVFHL----DFGK  304

Qy   526  A----TRQPIGVFGTMNSQYSDCDPLGNYA----------------PYLLLRKPGDQTEAAKATM  570
             |         |    :                         |||||||
Db   305  ALPSKDVTTDKDGI------SILDGIPHGTKVTITEKSVPDPYMIDTTPMAATIKAGETI  358

Qy   571  QDTYRATLERLFIDLEQERLLDRGAPCSSEGLS------SVIVDHPT--FRRILDTLRA  621
                                                         :  ::     :|||||:||
Db   359  SMTSKNMRQKGQILLEKTG-VETGTDLMNDNYSLAGNTFAIRKDSPAGEIVQEITTDEKG  417

Qy   622  RIEQTTQFMKVLVETRDYKIREGLSEATHSMALTFDP------YSGAFCPITNFLVKRT  675
                |||:      ||::|||||    :|          |        ||||:||||||||
Db   418  RAE--TPKELANALELGTYYVTE--TKSSNGFVNTFKPTKVELKYANQTVALVTSNVKGQ  473

Qy   676  HLAVVQDLAL-------------------SQCHCVFYGQQV------EGRNFRNQFQPVLRRRFVDL  717
             : : ::|                    :|             |:|       ::
Db   474  NQEITGETTLTKEDKDTGNESQGKAEFKGAEYTLFTAKDGQAVKWSEAFK------TEL  526

Qy   718  FNGGFISTRSITVTLSE-GPVSAPNPTLGQ--------DAPAGRTFDGDLARVSVE------  764
                                                               :  ::
Db   527  VKGTKASDEVTLALDEKNQVAVKHLAINEYFWQETKAPEGYTLDETKYPVSIKKVDNNE  586

Qy   765  ---VIRDIRVKNRVV--------------FSGNCTNLSEAA-------RARLVGLASAYQRQEKR  805
                |: :::                |:              |     |
Db   587  KNAVITRDVTAKEQVIRFGFDFFKFAGSADGTAETGFNDLSPXVSPLEGTXEITGAEDKA  646

Qy   806  VDMLHGALGP------------LLKQFHGLLFPRGM----PPNSKS----------PNP  838
             : ||                |                                |
Db   647  TTACNEQLGFDGYGKFENLPYGDYLLEEIEA--PEGFKITPLEIRSTFKENKDYAKS  703

Qy   839  QWFWTLLQRNQ------------MPADKLTHBEITTIAAVKRFTEBYAAINFINLP--PTCIGE  888
             :  :|:                ::|                            |:
Db   704  EYVFTITEBGQKQPIKMVTVPYEKLTNNB--------FSVSLNRLMLYDLPEKEDSLTS  754

Qy   889  LAQFYMANLILKYCDHSQYLINTLTSIITGARRPRDPSSVLHWIRKD---VTSAADIETQ  945
             ||    :         :| ||:|  |:::     |            |
Db   755  LATWKDGNKKLNTLDFTE-LVDKL----------------RYNLHEIKEDWYVVAQAIDVEA-  799

Qy   946  AKALLEKTENLPELWTTAFTST------------------HLVRAAMNQRPMVVLGISISKYHGA  992
             ||          |:                         |
Db   800  TKAAQEKDEKAKPVVIAETTATLANKEKTGTWKILHKLTAEQ------VLDKSIVLFNYV  853

Qy   993  AGNNRVFQAGNWSGLNGGKNVCPLFTPDRTRRPIIACPRGGFICPVTGPSSGNRETTLSD  1052
             |                                           :  :|::
Db   854  YENKVAFEAGNE----------------------------PVA-----KDASLNN  875

Qy   1053 QVRGIIVSGGAMVQLAIYATVVRAVGAR--------------AQHMAFDDWLSLTDDEFLARDL--  1102
                                                        |:
Db   876  QAQ----------------TVNCTIERHVSIQTKAHLEDGSQTFTHGDVMDMFDDVSVTHDVLD  923

Qy   1103 -BELHDQIIQTLETPWTTVEGALEAVKILDE--------------KTTAGD--GETPTNLAFNFD  1149
             :                                            :
Db   924  GSKEAFETILYALLPDGTNKEIWKSGKIEHEVNDKEPTKTVLAEKVDTGKYPEGTKFTF-  982

Qy   1150 SCEPSHDTTSNV----------------LNISGSNISGSTVPGLKRPPEDDE  1185
               ::: |                    |:::
Db   983  -TBINYEKDGNVANGKHNEDLKEKSQTLITPKEVPTIPSTPKQPE  1024
```

RESULT 6
US-09-071-035-394
; Sequence 394, Application US/09071035
; Patent No. 6448043
; GENERAL INFORMATION:
;   APPLICANT: Gil H. Choi
;   TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
;   NUMBER OF SEQUENCES: 496
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Human Genome Sciences, Inc.

```
Db   547  IVARREAVTAEHQ----LVAHAVALIAPGALPKTSSGKVRRRECRRAFLE----DALGER  598
               : :  :::     ||       :::           |: ::   :|   || ||
Qy   590  ------LLDRGAPCSSEGLSSVIVDHPTFRRILDTLRARIEQTTQFMKVLVETRDYKI  642
                 |||||||||||                    |:||||||
Db   599  HVAFAPELLDDASPPDD--APPETEEPSGRSLLDALRS---TLRALRLDAGQIDDAL  651

Qy   643  ---RBGL-SBATHSMALTFDPYSGAFCPITNFL  671
             |||  |||||||||||||||||||||||||||
Db   652  PISRFGLDSLAAVELQHAFQVRTGRAIPLTSIL  684
```

RESULT 5
US-09-071-035-358
; Sequence 358, Application US/09071035
; Patent No. 6448043
; GENERAL INFORMATION:
;   APPLICANT: Gil H. Choi
;   TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
;   NUMBER OF SEQUENCES: 496
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Human Genome Sciences, Inc.
;   STREET: 9410 Key West Avenue
;   CITY: Rockville
;   STATE: Maryland
;   COUNTRY: USA
;   ZIP: 20850
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
;   COMPUTER: HP Vectra 486/33
;   OPERATING SYSTEM: MSDOS version 6.2
;   SOFTWARE: ASCII Text
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/071,035
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:
;   FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: A. Anders Brookes
;   REGISTRATION NUMBER: 36,373
;   REFERENCE/DOCKET NUMBER: PB369P2
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (301) 309-8504
;   TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 358:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1074 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-09-071-035-358

Query Match   2.0%; Score 123; DB 4; Length 1074;
Best Local Similarity 18.3%; Pred. No. 0.016;
Matches 206; Conservative 150; Mismatches 415; Indels 352; Gaps 52;
```

```
Qy   250  RVRNVTAVARGAAHLAFDENHEGAVLPPDITVTYFQSSSSGTTTARGARRNDVNSTSKPS  309
                                          |:::::|||:
Db   67   RTTSLYAEYNGAKQTVFC-IEFGVSIFTEVTHGY---------------------QKNPL  104

Qy   310  PSGGFERRLASIM--AADTALHAEVIFNTGIYBE--------------TPTTDIKEWPMFI  353
                                |:|||                        ||
Db   105  PSMSDKAKLVSVLWEKAGTDIDTNMVAQKMIWEVNGYKLHSIKRLGGASVDIK-----  158

Qy   354  GMEGTLPRLNALGSYTAR------VAGVIG-AMVFSPNSALYLTEVEDSGMTBAKDGP  405
                                          |: :                ::
Db   159  SIEGKINK--AIEBYQKKPSFHNTTVKTILGQSTTLIDKNELNLSEFDKVVQNTA-----  211

Qy   406  GPSFNRFYQFAGPHLAANPQTDRDGHVLSSQSTGSSNTEFSVDYLALICGFGAPLLARLL  465
                                                  :||:
```

Qy   718 FNGGFISTRSITVTLSE-GPVSAPNPTLGQ------DAPAGRRTFDGDLLARVSVE------ 764
               ::|::| :|:| ||:| |:: |:
Db   527 VKGTKASDETVTLALDEKNQVAVCHLAINEYFWQETKAPEGYTLDETKYPVSIKKVDNNE 586

Qy   765 ---VIRDIRVKNRVV-------FSGNCTNLSEAA----------RARLVGLASAYQRQEKR 805
             :::||: | :| |::|:
Db   587 KNAVITRDVTAKEQVIRFGFDPFKFAGADGTAETGFNDLSFKVSPLEGTXEITGAEDKA 646

Qy   806 VDMLHGALGF-----------LLKQFHGLLFPRGM-----PPNSKS-----------PNP 838
               ||| ||| ||: | | | || | |||
Db   647 TTACNEQLGPDGYGKFENLPYGDYLLEEIEA---PEGFQKITPLEIRSTFKENKDDYAKS 703

Qy   839 QWFWTLLQRNQ-------MPADKLTHEITTIAAVKRPTEEYAAINFINLP--PTCIGE 888
              ||:|:|:|:| |: || | :|: ||:
Db   704 EYVFTITEBCQKQPIKMVTVPYEKLTNNE----------FSVSLNRLMLYDLPEKEDSLTS 754

Qy   889 LAQFYMANLLLKYCDHSQYLINTLTSIITGARRPRDPSSVLHWIRKD---VTSAADIETQ 945
               ||:: |:|| :| || | |: | : |::   :|
Db   755 LATWXDGNKKLNTLDFTE-LVDKL------------RYNLHEIKEDWTVVAQAIDVEA- 799

Qy   946 AKALLEKTENLPELWTTAFTST--------------HLVRAAMNQRPMVLGISISKYHGA 992
                 | | |::| |: | :: |: :| |
Db   800 TKAAQEKDEKAKPVVIAETTATLANKEKTGTWKILHKLTAEQ------VLDKSIVLFNTV 853

Qy   993 AGNNRVFQAGNWSGLNGGKNVCPLFTFDRTRRFIIACPRGGFICPVTGPSSGNRETTLSD 1052
               |::|| ||:| |:||||:| ||| |: | |::|||||:|| ||:|
Db   854 YENKVAFRAGNE-----------------------PVA----KDASLNN 875

Qy   1053 QVRGIIVSGGAMVQLAIYATVRAVGAR---------AQRMAFDDWLSLTDDEFLARDL- 1102
               | |:|| | ||:| :| |: | | ||: |:| : ||||::|||
Db   876 QAQ--------TVNCTIERHVSIQTKAHLEDGSQTFTHGDVMDMPDDVSVTHDVLD 923

Qy   1103 --EELHDQIIQTLETPWTVEGALEAVKILDE-------KTTAGD----GETPTNLAFNFD 1149
                ::|:||: |:| || ||:|:||:|:|| |:||| |:|
Db   924 GSKEAFETILYALLPDGTNKEIWKSGKIEHEVNDKEFTKTVLAEKVDTGKYPEGTKFTF- 982

Qy   1150 SCEPSHDTTSNV---------LNISGSNISGSTVPGLKRPPEDDE 1185
               |: |:|::| |:||| |:|:||||| |: |:||
Db   983 -TEINYEKDGNVNGKHNEDLKEKSQTLIPKEVPTIPSTPKQPE 1024

RESULT 7
US-09-134-000C-5764
; Sequence 5764, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5764
;   LENGTH: 1096
;   TYPE: PRT
;   ORGANISM: Enterococcus faecalis
US-09-134-000C-5764

Query Match   1.9%; Score 122; DB 4; Length 1096;
Best Local Similarity 18.5%; Pred. No. 0.02; Indels 410; Gaps 53;
Matches 208; Conservative 149; Mismatches 149;

Qy   250 RVRNVTAVARGAAHLAFDENHEGAVLPPDITYTYFQSSSGTTARGARRNDVNSTSKPS 309
               |::|: |:|||:|||:|||||||| |||: |:| |:::: | :||:|:|::|:|
Db   89 RTTSLYAEYNGAKQTVFC-IEPGVSIPTEVTHGY----------------QKNPL 126

Qy   310 PSGGFERRLASIM--AADTALHAEVIFNTGIYEE-----------TPTDIKEWPMFI 353
               ::|:| |:|:: ||||| |:|:| |:| | |||||||:||:|
Db   127 PSMSDKAKLVSVLWEKAGTDIDTNMVAQKMIWEEVNGYKLHSIKRLGGASVDIK----- 180

───

STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB369P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 394:
SEQUENCE CHARACTERISTICS:
LENGTH: 1074 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-071-035-394

Query Match   2.0%; Score 123; DB 4; Length 1074;
Best Local Similarity 18.3%; Pred. No. 0.016; Indels 415; Gaps 52;
Matches 206; Conservative 150; Mismatches 150;

Qy   250 RVRNVTAVARGAAHLAFDENHEGAVLPPDITYTYFQSSSSGTTARGARRNDVNSTSKPS 309
               |::|: |:|||:|||:|||||||||:|||::|::::: ||| :||:|:|::|:|
Db   67 RTTSLYAEYNGAKQTVFC-IEPGVSIPTEVTHGY----------------QKNPL 104

Qy   310 PSGGFERRLASIM--AADTALHAEVIFNTGIYEE-----------TPTDIKEWPMFI 353
               ::|:| |:|:: ||||| |:|:| |:|:| | |||||||:||:|
Db   105 PSMSDKAKLVSVLWEKAGTDIDTNMVAQKMIWEEVNGYKLHSIKRLGGASVDIK---- 158

Qy   354 GMEGTLPRLNALGSYTAR---------VAGVIG-AMVFSPNSALYLTEVEDSGMTEAKDGGP 405
               :|| ||| ||:|| || ::   :||:| |: |:||| || |||||
Db   159 SIEGKINK--AIBEYQKKPSFHNTTVKTLLGQSTTLIDKNELNLSBFDKVVQNTA----- 211

Qy   406 GPSFNRFYQFAGPHLAANPQTDRDGHVLSSQSTGSSNTEFSVDYLALICGFGAPLLARLL 465
               |:: | |: || |:|::   ::|:|:||: | |: |:
Db   212 ---NIDYRVIGNQLVLTP----------NSNSKSGTLTLKKSAGTGTP-VAYKK 251

Qy   466 FYLERCDAGAFTGGHGDALKYVTGTFDSEIPCSLCEKHTRPVCAHTTVHRLRQRMRFGQ 525
               |:|| ||| ||:|||:|:|||| ||| | |: ||:| | ||:||:|:|::||
Db   252 AGLQTVMAGALDKPNTYAIKINVETKGS-LKIKKIDKESGDIVPETVFHL------DFGK 304

Qy   526 A------TRQPIGVFGTMNSQYSDCDPLGNYA-----------PYLILRKPGDQTEAAKATM 570
                      ||:|:| |||::|:| |:|:||:| |::|||||||:||:||:|
Db   305 ALPSKDVTTDKDGI------SILDGIPHGTKVTITEKSVPDPYMIDTTPMAATIKAGETI 358

Qy   571 QDTYRATLERLFIDLEQERLLDRGAPCSSEGLS-----SVIVDHPT---FRRILDTLRA 621
               |:|:| | |::|| || |:| ||:|: |:||:|| ||:|||:|
Db   359 SMTSKNMRQKGOILLEKTG-VETGTDLWNDNYSLAGNTFAIRKDSPAGBIVQEITTDEKG 417

Qy   622 RIEQTTTQFMKVLVETRDYKIREGLSEATHSMALTFDP-------YSGAFCPITNFLVKRT 675
               |:|||: ||::| |:|:|:: | :|:|: |:| |:|: |:||:|| |:|
Db   418 RAE--TPKELANALGLGTYYVTE-TKSSNGFVNTFKPTKVELKYANQTVALVTSNVKGQ 473

Qy   676 HLAVVQDLAL--------SQCHCVFYGQQV------EGRNFRNQFQPVLRRRFVDL 717
               ||: | | |:| | |:   :|||:|::|::|||:||::||
Db   474 NQEITGETTLITKEDKDTGNESSQGKAEFKGAEYTLFTAKDGQAVKWSEAFK------TEL 526

```
; Patent No. 6551795
; GENERAL INFORMATION:
;   APPLICANT: Rubenfield et al.
;   APPLICANT: Marc J.
;   TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;   TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;   FILE REFERENCE: 107196.136
;   CURRENT APPLICATION NUMBER: US/09/252,991A
;   CURRENT FILING DATE: 1999-02-18
;   PRIOR APPLICATION NUMBER: US 60/074,788
;   PRIOR FILING DATE: 1998-02-18
;   PRIOR APPLICATION NUMBER: US 60/094,190
;   PRIOR FILING DATE: 1998-07-27
;   NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 16913
;   LENGTH: 370
;   TYPE: PRT
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16913

  Query Match             1.9%;  Score 118.5;  DB 4;  Length 370;
  Best Local Similarity   20.2%;  Pred. No. 0.0061;
  Matches   93;  Conservative  46;  Mismatches 137;  Indels 185;  Gaps  19;

Qy  208 PDPFNTHHRSIGEGFVYPTPFYNTGLCHLIHDCVIAPMAVALRVRNVTAVARGAAHLAFD 267
         |||  :
Db   17 PDPCNAYH----------------------------------------------TDEQRWAAVLTRD 37

Qy  268 ENHEGA-VLPPDITYTYFQSSSSGTTTARGARRNDVN--STSKPSPSGGF-------ER 316
               :       :
Db   38 AAADGAFVYAVKTTGVYCRPSSS---ARRPRRENVEFFATAEAAEAAGYRPSRRAAGDR 93

Qy  317 RLASIMAADTALHAEVIFNTGIYEETPTDIKEWPMFIGME------------GTLPRLNA 364
Db   94 RLAAEQRAERVAQACRMIETA----ETPPALEALAARLGMSPFHFHRLFKAETGLTPKAVA 150

Qy  365 LGSYTARVAGVIGAMVFSPNSALYLTEVEDSGMTEAKDGGPGPSFNRFYQFAGPHLAANP 424
Db  151 SAYRARRLRERLGQASASVTEAIY-------DSGFN-----------SNSRFYESSSQRLGMRP 196

Qy  425 QTDRDGHVLSSQSTGSSNTEFSVDYLALICGFGAPLLARLLFYLERCDAGAFTGGHGDAL 484
Db  197 RDYRDG---------------------GAG--------AAIRFAIGQCSLGAI-------- 220

Qy  485 KYVTGTFDSEIPCSLCEKHTRPVCA-------------HTTVHRLRQRMPR--------FGQATR 528
Db  221 -------------LVAQSQRGICAILLGEEPEPLLRELQDQPPRAQLLGGDADFERLVA 266

Qy  529 QPIGVFGTMNSQYSDCDPLGNYAPYLLLRKPGDQTEAKATMQ------DTYRATLERLF 582
Db  267 QVVG----FVESPQLGLDLP-LDVRGTAFQERVWQALREIPPGSTASYAQIAERI- 316

Qy  583 IDLEQERLLDRGAP-----------CSSEGLSSVIVDHPFPRR 614
Db  317 -----------GAPRAVRAVAQACAANRIAVAIPCHRVVRR 346


RESULT 9
US-09-489-039A-12681
; Sequence 12681, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
;   APPLICANT: Gary Breton et. al
;   TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
;   TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
;   FILE REFERENCE: 2709.2004001
;   CURRENT APPLICATION NUMBER: US/09/489,039A
;   CURRENT FILING DATE: 2000-01-27
;   PRIOR APPLICATION NUMBER: US 60/117,747
;   PRIOR FILING DATE: 1999-01-29
;   NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12681
;   LENGTH: 855
;   TYPE: PRT
```

```
Qy  354 GMEGTLPRLNALGSYTAR-----------VAGVIG-AMVFSPNSALYLTEVEDSGMTEAKDGGP 405
Db  181 SIEGKINK--AIEEYQKKPSFHNTTVKTILGQSTTLIDKNELNLSEFDKVVQNTA------- 233

Qy  406 GPSFNRFYQFAGPHLAANPQTDRDGHVLSSQSTGSSNTEFSVDYLALICGFGAPLLARLL 465
Db  234 ----NIDYRVIGNQLVLTP---------------NSNSKSGTLTLKKSAGTGTP-VAYKK 273

Qy  466 FYLERCDAGAFTGGHGDALKYVTGTFDSEIPCSL-----CEKHTRPVCAHTTVHRLRQRMP 521
Db  274 AGLQTVMAGALDKPNTYAIK-----IDVETKGSLKIKKKIDKESGDIVPETVFHL------ 322

Qy  522 RFGQA-----------TRQPIGVFGTMNSQYSDCDPLGNYA-----------PYLILRKPGDQTEAA 566
Db  323 DFGKALPSKDVTTDKDGI---------SILDGIPHGTKVTITEKSVPPDYMIDTTPMAATIKA 376

Qy  567 KATMQDTYRATLERLFIDLEQERLLDRGAPCSSEGLS-----------SVIVDHPT---FRRILD 617
Db  377 GETISMTSKNMRQKGQILLEKTG-VETGTDIWNDNYSLAGNTFAIRKDSPAGEIVQEITT 435

Qy  618 TLRARIEQTTQFMKVLVETRDYKIREGLSEATHSMALTFDP-------YSGAFCPITNFL 671
Db  436 DEKGRAE--TPKELANALELGTYYVTE--TKSSNGFVNTFKPTKVELKYANQTVALVTSN 491

Qy  672 VKRTHLAVVQDLAL------------SQCHCVFYGQQV-----------EGRNFRNQFQPVLRRR 713
Db  492 VKGQNQEITGETTLTKEDKDTGNESQGKAEFKGAEYTLFTAKDGQAVKWSEAFK------- 545

Qy  714 FVDLFNGGFISTRSIITVTLSE-GPVSAPNPTLGQ-----------DAPAGRTFDGDLARVSVE-- 764
Db  546 -TELVKGTKASDETVTLALDEKNQVAVKHLAINEYFWQETKAPEGYTLDETKYPVSIKKV 604

Qy  765 -----------VIRDIRVQNRVV------FSGNCTNLSEAA-----------RARLVGLASAYQR 801
Db  605 DNNEKNAVITRDVTAKEQVIRFGFDFFKFAGSADGTAETGFNDLSFKVSPLEGTNEITGA 664

Qy  802 QEKRVDMLHGALGF-----------LLKQFHGLLFPRGM---PPNSKS----------- 835
Db  665 EDKATTACNEQLGFPDGYGKFENLPYGDYLLEEIEA--PEGFQKITPLEIRSTFKENKDD 721

Qy  836 -PNPQWFWTLLQRNQ-----------MPADKLTHEBITTIAAVKRFTEBYAAINFINLP--PT 884
Db  722 YAKSEYVFTITEEGQKQPIKMVTVPYEKLTNNE-----FSVSLNRIMLYDLPEKED 772

Qy  885 CIGELAQFYMANLILKYCDHSQYLINTLTSIITGARRPRDPSSVLHWIRKD---VTSAAD 941
Db  773 SLTSLATWKDGNKKLNTLDFTE-LVDKL-----------RYNLHEIKEDWYVVAQAID 818

Qy  942 IETQAKALLEKTENLPELWTTAFTST---------------HLVRAAMNQRPMVVLGISISK 988
Db  819 VEA-TKAAQEKDEKAKPVVIAETTATLANKEKTGTWKILHKLTAEQ----VLDKSIVL 871

Qy  989 YHGAAGNNRVFQAGNWSGLNGGKNVCPLFTFDRTRRFIIACPRGGFICPVTGPSSGNRET 1048
Db  872 FNYVYENKVAFEAGNE-----------PVA------KDA 893

Qy 1049 TLSDQVRGIIVSGGAMVQLAIYATVVRAVGAR-----------AQHMAFDDWLSLTDDEFLAR 1100
Db  894 SLNNQAQ---------TVNCTIERHVSIQTKAHLEDGSQTFTHGDVMDMFDDVSVTH 941

Qy 1101 DI----EELHDQIIQTLETPWTVEGALEAVKILDE-----------KTTAGD---GETPTNLA 1145
Db  942 DVLDGSKEAFETILYALLPDGTNKEIWKSGKIEHEVNDKEFTKTVLAEKVDTGKYPEGTK 1001

Qy 1146 FNFDSCEPSHDTTSNV-----------LNISGSNISGSTVPGLKRPPEDDE 1185
Db 1002 FTF--TEINYEKDGNVNGKHNEDLKEKSQTLTPKEVPTIPSTPKQPE 1046


RESULT 8
US-09-252-991A-16913
; Sequence 16913, Application US/09252991A
```

```
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12681

Query Match          1.9%;   Score 117;  DB 4;  Length 855;
Best Local Similarity   21.8%;  Pred. No. 0.042;
Matches  107;  Conservative  54;  Mismatches 140;  Indels 190;  Gaps  29;

Qy   51 NLTVEKTFISSLAVV-------------SGARTGLAGAGITLKLTSHFYPSVFVFHGGGKHVLP 102
        :||:                        :: ||||:|||  ::|:||:|:|||||.|:
Db  166 SLTVDAAQSSLVAHLACESLRAGESTTALV-AGVNL------------------------NILA 206

Qy  103 SSAAPNLTRACNAARERFGFSRCQQPPVDGAVETTGAEICTRLGLEPENTLLYLVVTALF 162
        |||:                                                 ::||:|
Db  207 ESA------------------------VTEERFG-------------------GLSPDGTAYTFDARA-- 231

Qy  163 KEAVFMCNVFLHYGGLDIVHINHGDVIRIPLFPVQLFMPDVNRLVPDPFNTHHRSIGEGF 222
              :|:            :|          ||.|                  |
Db  232 ------NGFVRGEG---------GGVVLKPL----------------SRALADGDRVH------GV 261

Qy  223 VYPTPFYNTGLCHLIHDCVIAPMAVALRVRNTVARGAAHLAFDENHEGAVLPPDITYT 282
                                 ::|                 |
Db  262 IRASAVNNDG-------------ATPGLTVPSRAQEKVLREAYRKAALDPS-AVQ 303

Qy  283 YFQSSSSGTTARGARRNDVNSTSKPSPSGFERRLASIMAADTALHAEVIFNTGIYEET 342
        |:                 |: :|                           ||.|
Db  304 YVELHGTGT-------------PVGDPIEAAALGAVLGSARPADEPL--------LVGSA 342

Qy  343 PTDIKEWPMFIGMEGTLPRLNALGSYTARVAGVIGAMVFSPNSALYLTEVEDSGMTEAKD 402
                   |||:                                :||
Db  343 KTNVGHLEGAAGIVGLIKTLLALG--RRRIPASLNFRTPHDIPL------DTLGLDVPD 394

Qy  403 GGPGPSFNRFYQFAGPHLAANPQTDRD---------------GHVLSSQSTGSSNTEFSVD 448
        |                                         ||:
Db  395 G-------------LREWPHPDRELLAGVSSFGMGGTNAHVVLSEGPAQGGEQPGID 438

Qy  449 YLIALICGFGAPLLARLLFYLERCDAGA-------FTGGHGDALK--------YVTGTFDSEI-P 496
        |:                           ::||                    :
Db  439 EETPV---------------DSGAALPFVVTGRGGEALRAQARRLHEAVEADPELAP 480

Qy  497 CSLCEK--HTRPVCAHTTV------HRLRQRMRPFGQATRQPIGVFGTMNSQYSDCDPLG 548
           :                      |                     :||
Db  481 AALARSLVTTRTVFTHRSVVLAPDRARLLDGLGLAAAGTPAPGVVTGT---------528

Qy  549 NYAPYLILRKPGDQTEAAKATMQDTYRATLERLFIDLEQERLLDRGAPCSSEGLSSVIVD 608
                                   |                         :||
Db  529 ---------PAPG---------RLAVLF---------------SGQGAQRTGMGM-ELYAA 555

Qy  609 HPTFRRILDTLRARIEQTTTQFMKVLVETRD---------------YKIREGLSEATHSMALT 656
        || |                                          |:
Db  556 HPAFA-AFDAVAAELDPLLDRPLAEIVAAGTLDRTVHTQPALFAVEVALHRLVESWGVT 615

Qy  657 FDPYSGAFCPITNFLVKRTHLAVVQDLALSQCHCVFYGQQVEGRNFRNQFQPVLRRRFVD 716
        |                        |:                 :::|
Db  616 PDLLAGH-----SVGEISAAHVAGV--LSLRDA------ARLVAARGRLMQALP-------656

Qy  717 LFNGGFISTRSITVTLSEGPVSAPNPTLGQDAPAGRTFDGDLARVSVEVIRDIRVKNRVV 776
                 |:                                  |:
Db  657 --EGGAM-----VAVEASEEEVL---PHL------AGRERELSLAAVN---------GPRAVV 694

Qy  777 FSGNCTNLSEAARARIVGLASAYQRQEKRVDMLHGALGFLLKQFHGLLF----------825
        | |                                               :|:
Db  695 LAG-------AERAVLDVAELLREQGRRTKRLLSVSHA----------FHSPLMEPMLDDFRRVV 741

Qy  826 ---------PR------GMPPNSKSPNPQW---FWTLLQRNQMPADKLTHEEITTIAAV 866
                 ::                                   :|
Db  742 EELDFQEPRVDVVSVTVGLPVTA----GQWTDPEYW-----VDQV-RRPVRFLDAV 787

Qy  867 KRFTEEYAAINFINLPP--TCIGELAQFYMANLILKYCDHSQYLINTLTSIITGARRPRD 924
        ||:                                                  :|:|-E
Db  788 -RTLEESGADTFLELGPDGVCSAMAADSV---------RDQEAATAVSALRKG--RP-E 833

Qy  925 PSSVLHWIRKDVTSAADIETQAKALLEKTENLPELWTTAFTSTHLVRAAMNQRPMVVLGI 984
        | :                                                :|
Db  834 PQSLLAALTTVFVRGHDVD---------------WTAAHGSTGTVRVPL--PTYAFQR 874

Qy  985 SISKYHGAAGNRVFQAGNWSGLNGGKNVCPLFTFDRTRRPIIACPRGGFICPVTGPSSG 1044
        : :|                                              |||:
Db  875 ERHWFDGAARTAAPLTAGR-SGTGAG---------------TGPAAG 905

Qy 1045 NRETTLSDQVRGIIVSGGAMVQLAIYATVVRA-VGARA 1081
```

```
Query Match          1.8%;   Score 111;  DB 4;  Length 4630;
Best Local Similarity   19.7%;  Pred. No. 4.2;
Matches  250;  Conservative 109;  Mismatches 419;  Indels 494;  Gaps  66;
```

```
Qy  497  CSLCEK--HTRPVCAHTTV-------HRLRQRMPRFGQATRQPIGVFGTMNSQYSDCDPLG  548
               : :                  : ||                    :::     ||
Db  481  AALARSLVTTRTVFTHRSVVLAPDRARILDGLALAGTPAPGVVTGT-----------  528

Qy  549  NYAPYLILRKPGDQTEAAKATMQDTYRATLERLFIDLEQERILLDRGAPCSSEGLSSVIVD  608
                                                                  ||
Db  529  -----------PAPG-----------RLAVLF--------SGQAQRTGMGM-ELYAA  555

Qy  609  HPTFRRILDTLRARIEQTTQFMKVLVETRD------YKIREGLSEATHSMALT  656
         ||  :         :      :       ::               :::
Db  556  HPAFATAFDAVAAELDPLLDRPLAELVAAGDTLDRTVHTQPALFAVEVALHRLVESWGVT  615

Qy  657  FDPYSGAFCPITNFLVKRTHLAVVQDIALSQCHCVFYGQQVEGRNFRNQFQPVLRRRFVD  716
          ||       :         :  ::    :           :
Db  616  PDLLAGH---SVEISAAHVAGV--LSLRDA----ARLVAARGRLMQALP--------  656

Qy  717  LFNGGFISTRSITVTLSEGPVSAPNPTLGQDAPAGRTFDGDLARVSVEVIRDIRVKNRVV  776
                             ::                     ||  :
Db  657  --EGGAM---VAVEASEEVL--PHL----AGRERELSLAAVN------GPRAVV  694

Qy  777  FSGNCTNLSBAARARLVGLASAYQREKRVDMLHGALGFLLKQFHGLLP-------------  825
                   :::  :           ::: :
Db  695  LAG-----AERAVLDVAELLREQGRRTKRLSVSHA---------FHSPLMEPMLDDFRRVV  741

Qy  826  --------PR-----GMPPNSKSPNPQW----FWTLLQRNQMPADKLTHEITTIAAV  866
                          :                    :
Db  742  BELDFQEPRVDVVSTVTGLPVTA---GQWTDPEYW--------VDQV-RRPVRFLDAV  787

Qy  867  KRFTEEYAAINFINLPP--TCIGELAQFYMANLILKYCDHSQYLINTLTSIITGARRPRD  924
                                        ::::          :::
Db  788  -RTLEBSGADTFLELGPDGVCSAMAADSV-----------RDQEAATAVSALRKG--RP-E  833

Qy  925  PSSVLHWIRKDVTSAADIETQAKALLEKTENLPELWTTAFTSTHLVRAAMNQRPMVVLGI  984
              :  :  :                              ::
Db  834  PQSLLAALTTVFVRGHDVD------------WTRAHGSTGTVRVPL---PTYAFQR  874

Qy  985  SISKYHGAAGNNRVFQAGNWSGLNGGKNVCPLFTFDRTRRFIIACPRGGFICFVTGPSSG 1044
               :                                     :          ||
Db  875  ERHWFDGAARTAAPLTAGR-SGTGAG------------TGPAAG  905

Qy 1045  ----------------------NRETTLSDQVRGIIVSGGAMVQLAIYATVVRA-VGARA 1081
                                       :                   :   :
Db  906  VTSGEGEGEGAGAGGGDRPARHETT----VLEYDDPTRVELGLTF  957

Qy 1082  QHMAFDDWLS------LTDDEFLARDLEELHDQIIQTLETPWTVEGALEAVKILDEKTTA 1135
              : :       :||       ||       ||      ||
Db  958  KELGFDSLMSVELRNALVDDTGLRLPSGLLFDH----RALAA--HLGDLLTG 1006

Qy 1136  GDGETPTNLAFNFDSCEPS--HDTTSNVLNISGSNISGSTVPGLKRPEDDELFDL---- 1189
         ||||                 ||        ||         : |  ||
Db 1007  GSGETG-----SADGIPPATPADTTAEPIAIIG---MACRYPGGVTSPED--LWRLVAEG 1056

Qy 1190  ----SGIPIKHG 1197
             |||
Db 1057  RDAVSGLPTDRG 1068
```

```
Db  906  VTSGEGEGEGAGAGGGDRPARHETT----VLEYDDPTRVELGLTF  957
              :                   :          :
Qy 1082  QHMAFDDWLS------LTDDEFLARDLEELHDQIIQTLETPWTVEGALEAVKILDEKTTA 1135
Db  958  KELGFDSLMSVELRNALVDDTGLRLPSGLLFDH----RALAA--HLGDLLTG 1006
Qy 1136  GDGETPTNLAFNFDSCEPS--HDTTSNVLNISGSNISGSTVPGLKRPEDDELFDL---- 1189
Db 1007  GSGETG-----SADGIPPATPADTTAEPIAIIG---MACRYPGGVTSPED--LWRLVAEG 1056
Qy 1190  ----SGIPIKHG 1197
Db 1057  RDAVSGLPTDRG 1068
```

RESULT 11
US-10-105-537-2
; Sequence 2, Application US/09105537A
; Patent No. 6265202
; GENERAL INFORMATION:
; APPLICANT: Sherman, D.H.
; APPLICANT: Xue, Y.
; APPLICANT: Zhao, L.
; TITLE OF INVENTION: DNA encoding methymycin and pikromycin
; FILE REFERENCE: 600.438US1
; CURRENT APPLICATION NUMBER: US/09/105,537A
; CURRENT FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 5215
; TYPE: PRT
; ORGANISM: Streptomyces venezuelae
US-09-105-537-2

```
Query Match          1.8%;  Score 111;  DB 3;  Length 5215;
Best Local Similarity 19.7%;  Pred. No. 5.2;
Matches  250;  Conservative 109;  Mismatches 419;  Indels 494;  Gaps  66;

Qy   51  NLTVEKTFTSSLAVV---------SGARTTGLAGAGITLKLTTSHFYPSVFVFHGGKHVLP  102
         ||:::   ::||      :: ||
Db  166  SLTVDAAQSSSILVAVHLACBSLRAGESTTALV-AGVNL---------------NILA  206

Qy  103  SSAAPNLTRACNAAERFRGFSRCQGPPVDGAVETTGAEICTRLGLEPENTILYLVVTALF  162
                                                           :
Db  207  ESA--------VTEERFG----------GLSPDGTAYTFDARA--  231

Qy  163  KEAVFMCNVFLHYGGLDIVHINHGDVIRIPLFPPVQLFMPDVNRLVPDPFNTHHRSIGEGF  222
              :                |:|                  ||
Db  232  ----------NGFVRGEG-----GGVVVLKPL----------SRALADGDRVH------GV  261

Qy  223  VYPTPFYNTGLCHLIHDCVIAPMAVALRVRNVTAVARGAAHLAFDENHEGAVLPPDITYT  282
                                    ||
Db  262  IRASAVNNDG---------ATPGLTVPSRAAQBKVLREAYRKAALDPS-AVQ  303

Qy  283  YFQSSSSGTTARGARRNDVNSTSKPSPSGGFERRLASIMAADTALHAEVIFNTGIYEET  342
         ||                                           ||
Db  304  YVELHGTGT-----------PVGDPIEAAALGAVLGSARPADEPL----------LVGSA  342

Qy  343  PTDIKEWPMFIGMEGTLPRLNALGSYTARVAGVIGAMVFSPNSALYLTEVEDSGMTEAKD  402
            :                ||  ||         ::        ::|:||
Db  343  KTNVGHLEGAAGIVGLIKTLLALG--RRRIPASLNFRTPHPDIPL------DTLGLDVPD  394

Qy  403  GGPGPSFNRFYQFAGPHLAANPQTDRD---------GHVLSSQSTGSSNTBFSVD  448
         ||                          :||
Db  395  G---------LREWHPDRELLAGVSSFGMGGTNAHVVLSEGPAQGGEQPGID  438

Qy  449  YLALICGFGAPLLARLLFYLERCDAGA-----FTGGHGDALK-----YVTGTFDSEI-P  496
          :|||                             :||
Db  439  EETPV----------DSGRALPFVVTGRCGEALRAQARRLHEAVEARDPELAP  480
```

RESULT 12
US-09-543-681A-6059
; Sequence 6059, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 6059
; LENGTH: 790

; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-6059

```
Query Match          1.7%;   Score 110;  DB 4;  Length 790;
Best Local Similarity   19.1%;   Pred. No. 0.19;
Matches 171;  Conservative 124;  Mismatches 350;  Indels 250;  Gaps 42;

Qy   350  PMFIGMEGTL-----------------PRLNALGSYTARVAGVIGAMVFSPN  384
              |:|||  |
Db    34  PLFVGREKSIHCLEAAMNDNKQIMLVAQKDASTDEPGVNDLFS-VGTVASVLQMLKLPDG   92

Qy   385  SALYLTE-VEDSGMTEAKDCGPGPSFNRFYQFAGPHLAANPQTDRDGHVLSSQSTGSSNT  443
                         ::|:|            :|:|
Db    93  TVKVLVEGIRRAKITTLSDNG-----------EYFQAKAEYLDTPVVDEREQEVLNR----TAIN  142

Qy   444  EFSVDYLALICGFGAPLLARLLFYLERCDAGAFTGGH-----------------GDALKY  486
                       :::|
Db   143  QFE-GYIKLNKKIPPEVLASLHAIEBSAKLADTIASHMPLKLKDKQAVLEMSDVTERLEY  201

Qy   487  VTGTFDSEIPCSLCEKHTRPVCAHTTVHRLRQRMPR------FGQATRQPIGVFGTMNSQ  540
                 |:||
Db   202  LMAMMESEIDLLQVEKRIR--------NRVKKQMEKSQREYLNEQMKAIQKELGEMDDA   253

Qy   541  YSDCDPLGNYAPYLILRKPGDQTEAAKAIMQD--------TYRATLERLFIDLEQERLLDR  593
                                     ::|:|
Db   254  PDEMSLKRKIE--AAKMPKEAREKTEAELQKLKMMSPMSAEAATVVRSYIDWMVQ-----  306

Qy   594  GAPCSSEGLSSVIVDHPTFRRILDTLRARIEQTTTQFMKVL-VETRDYKIREGLSEATHS  652
                |:|
Db   307  -VPWNSR--SKVKKDLVKAQEVLDTDHYGLERVKERILEYLAVQSRVSKIKGPI------  357

Qy   653  MALTFDPYSG------AFCPITNFLVKRTHLAVVQDLALSQCHCVFYGQQVEGRNFRNQF  706
                                        ::
Db   358  LCLVGPPGVGKTSLGQSIAKATGRKYVRMALGGVRDEA------------EIRGH----  400

Qy   707  QPVLRRRFVDLFNGGFISTRSITVTLSEGPVSAFNPTLGQDAPAGRTFD--GDLARVSVE  764
                                                :::|
Db   401  ----RRTYIGSMPGKLIQKMA---------KVGVKNPLFLLDEIDKMSSDMRGDPASALLE  448

Qy   765  VI---RDIRVKNR----------------VVFSGNCTNLSEAA----RARLVGLASAYQRQEKRVD  807
              |:   |:                            ::|
Db   449  VLDPEQNIAFNDHYLEVDYDLSDVMFVATSNSMNIPAPLLDRMEVIRL-SGYTEDEK---  504

Qy   808  MLHGALGFLL-KQFHGLLFPRGMPPNSKSPNPQWFTLLQRNQMPADKLTHEBITTIAAV  866
              ||||
Db   505  -LNIAKQHLLPKQ----------------------IERNALKENELTIHDSAIMGII   538

Qy   867  KRFTEBYAAINFI--NLPPTCIGELAQFYMANLILKYCDHSQYLINTLSIITGARRPRD  924
              :||
Db   539  RYYTRE-AGVRSLEREISKLCRKAVKQLLMDSTI----KHIBIDENNLKDYL-GVRK---  589

Qy   925  PSSVLHWIRKD------VTSAADIETQAKALLEKTENLPELWTTAPT-STHLVRAAMNQ  976
              :|
Db   590  ----VDYGRADTENRIGMVTGLAWTEVGGDLLTIETASVPCKGKLFTGSLGEVMQESIQ  645

Qy   977  RPMVVLGISISKYHGAAGNNRVFQAGNMWSGLNGGKNVCPLFTFDRTRRFIIACPRGGFIC 1036
              ::
Db   646  AAMTVVRARADKL-----------------GING------DFYEKRDIHVHVPEGA--T  679

Qy  1037  PVTGPSSGNRETT------LSDQVRGIIVSGGAMVGLAIYATVVRAVGAR------AQHMAF 1086
              :|
Db   680  PKDGPSAGIAMCTALVSSLTGNPVRSDVAMTG--EITLRGQVLPIGGLKEKLLAAHRGG  736

Qy  1087  IKTVLIPDEN--KRDLEEIPENIVADID------IHPVKTIEEVLTLALEKSP  781
              :|:
Db   737  DDWLSLTDDEFLARDLELHDQIIQTLETPWTVEGALEAVKILDEKTAGDGETP 1141
```

RESULT 13
US-07-642-734C-4
; Sequence 4, Application US/07642734C
; Patent No. 5824513

```
Query Match          1.7%;   Score 106.5;  DB 2;  Length 3567;
Best Local Similarity   19.9%;   Pred. No. 7.4;
Matches 237;  Conservative 104;  Mismatches 384;  Indels 465;  Gaps 62;

Qy   125  CQGPPVDGAVETTGAE--ICTR---------LGLEPENTILYLVVTALFKKRAVFMCNVFLH  174
              ::  ::|::::|||        :
Db  1165  CPGDDLLAAVEEAGASAVVCAQDAAALREALGDEP-------------------VTAL----VH 1205

Qy   175  YGGLDIVHINHGDVIRIPLFPPVQLFMPDVNRLVPDPFNTHHRSIGEGFVVPTPFVNTGLC  234
              ::|
Db  1206  AGTL---TNFG----------------SISEVAPEEF----------AETIAAKTALL  1234

Qy   235  HLIHDCVIAPMAVALRV------------------RNVTAVARGAAHL-AFDENHEGAVLPPDITYT 282
                                           :::|:|
Db  1235  AVL-DEVLGDRAVEREVYCSSVAGIWGGAGMAAYAAGSAYLDALAEHHR----------------1282

Qy   283  YFQSSSSGTTTARGARRNDVNSTSKPSPSG----GF--ERRLASIMAADTALHA-EVIFN  335
                                              :|
Db  1283  -----------ARGRSCTSVAWTPWALPGGAVDDGYLRERGLRS-LSADRAMRTWERVLA  1330

Qy   336  TGIYEBTPDIKEWPMFI-GMEGTLPRLNALGSYTARVAGVIGAMVFSPNSALYLTEVED  394
                                       :::|::|:
Db  1331  AGPVSVAVADV-DWPVLSEGFAATRP---------------------TALFAELAGR  1365

Qy   395  SGMTEAKDGGPGPSFNRFYQFAG----------PHLAANPQTDRDGHVLSSQSTGSSNTE 444
              ::|::|
Db  1366  GGQAEAEPDS-GPTGEPAQRLAGLSPDEQQENLLELVANAVAE---VLGHESAAEINVR 1420

Qy   445  FSVDYLALICGFGAPLLARLLFYLERCDAGAFTGGHGDALKYVTGTFDSEIPCSLCEKHT  504
                           :::|
Db  1421  RAFSELGLDSLNAMALRKRL----------SASTG------LRLPASL----  1452

Qy   505  RPVCAHTTVHRLRQ--RMPRFGQATRQPIGVFGTMNSQYSDCDPL-----------------GNYA 551
              | |:   |:
```

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/439,009A
FILING DATE: 11-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Casuto, Dianne
REGISTRATION NUMBER: 40,943
REFERENCE/DOCKET NUMBER: 4952.US.DI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-938-3137
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3567 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-439-009A-4

Query Match   1.7%;   Score 106.5;   DB 3;   Length 3567;
Best Local Similarity 19.9%;   Pred. No. 7.4;
Matches 237; Conservative 104; Mismatches 384; Indels 465; Gaps 62;

```
Qy   125 CQGPPVDGAVETTGAE--ICTR--------LGLEPENTILYLVVTALFKGAVFMCNVFLH 174
Db  1165 CPGDDLLAAVEEAGASAVVCAQDAAALREALGDEP----------------VTAL----VH 1205
Qy   175 YGGLDIVHINHGDVIRIPLFPVQLFMDVNRLVPDFNTHRSIGEGFVYPTFPYNTGLC 234
Db  1206 AGTL--TNFG-------------SISEVAPEEP----------------AETIAAKTALL 1234
Qy   235 HLIHDCVIAPMAVALRV-----------RNVTAVARGAAHL-AFDENHEGAVLPPDITYT 282
Db  1235 AVL-DEVLGDRAVEREYCSSVAGIWGGAGMAAYAAGSAYLDALAEHHR---------- 1282
Qy   283 YFQSSSGTTTARGARRNDVNSTSKPSPSG----GF--ERRLASIMAADTALHA-EVIFN 335
Db  1283 ----------ARGRSCTSVAWTPWALPGGAVDDGYLRERGLRS-LSADRAMRTWERVLA 1330
Qy   336 TGIYEETPTDIKEWPMFI-GMEGTLPRLNALGSYTARVAGVIGAMVFSPNSALYLTEVED 394
Db  1331 AGPVSVAVADV-DWPVLSEGFAATRP---------------------TALFAELAGR 1365
Qy   395 SGMTEAKDGGPGPSFNRFYQFAG---------PHLAANPQTDRDGHVLSSQSTGSSNTE 444
Db  1366 GGQAEAEPDS-GPTGEPAQRLAGLSPDEQQENLLELVANAVAE---VLGHESAAEINVR 1420
Qy   445 FSVDYLALICGFGAPLLARLLFYLERCDAGAFTGGHGDALKYVTGTFDSEIPCSLCEKHT 504
Db  1421 RAFSELGLDSLNAMALRKRL-------------SASTG----------LRLPASL----- 1452
Qy   505 RPVCAHTTVHRLRQ--RMPRFGQATRQPIGVFGTMNSQYSDCDPL-----------GNYA 551
Db  1453 --VFDHPTVTALAQHLRARLVGDADQAAVRVVGAAD---ESEPIAIVGIGCRFPGGIGS 1506
Qy   552 PYLILR-----------------------------KPGDQTEAA------------ 566
Db  1507 PEQLWRVLAEGANLTTGFPADRGWDIGRLYHPDPDNPGTSYVDKGGFLTDAADFDPGFFG 1566
Qy   567 ----------KATMQDTYRATLERLFIDLEQERLLDRGAPCSSEGLSSVIVDHPTFRR 614
Db  1567 ITPREALAMDPQQRLMLETAWEAVERAGIDPDALRGTDTGVFVGMNGQSYMQLLAGEAER 1626
Qy   615 I-----------LDTLRARIEQT----------TTQFMKVLVETRDYKIREGLSEATHSMAL 655
Db  1627 VDGYQGLGNSASVLSGRIAYTFGWEGPALTVDTACSSSLVGI--HLAMQALRRGECSLAL 1684
Qy   656 T-----FDPYSGAFCPITNFLVKRTHLAVVQDLALSQCHCVFYGQQVEGRNFRN----- 704
Db  1685 AGGVTVMSDPYT-------FVDFSTQR------GLA-SDGRCKAFSARADGFALSEGVAAL 1731
Qy   705 QFQPVLRRRFVDLFNGGFISTRSITVTLSEGPVSAPNPTLGQDAPAG----RTFDGDLAR 760
```

```
              TYPE: AMINO ACID
              TOPOLOGY: linear
              MOLECULE TYPE: protein
              HYPOTHETICAL: NO
              ORIGINAL SOURCE:
                ORGANISM: Pseudomonas species
                STRAIN: SE83
US-07-731-157A-7

Query Match             1.7%;  Score 106;  DB 1;  Length 774;
Best Local Similarity  20.2%;  Pred. No. 0.47;
Matches 145;  Conservative 79;  Mismatches 251;  Indels 242;  Gaps 37;

Qy  258 ARGAAHLAFDENHEGAV-LPPDITYTYFQSSSGTTARGARRNDVNSTSKPSPSGGFER   316
            :|| :. .:|:.  ::|::     | .:|||  .  .:.  :.|
Db  183 AANALKLRYDDGGQDLLCIPPGVEAERLEADLALRPAVDALLKAMGGDASDAAGGGSNN   242

Qy  317 ------RLAS--IMAADTALHAEVIFNTGIYEETPTDIKEWPMFIGMEGTLPRLNALGS   367
              ||.:   :| ||:|| | :: ||:||:|||:|::|| :|:: .::|
Db  243 WAVAPGRTATGRPILAGDPHRVFEI---PGMYAQHHLACDRFDM-IGL--TVP------   289

Qy  368 YTARVAGVIGAMVFSPNSA------------------LYLTEVEDSGMTE--------   399
                                                 |
Db  290 ------GVPGFPHFAHNGKVAYCVTHAFMDIHDLYLEQFAEDGRTARFGNEFEPVAWRRD  343

Qy  400 --AKDGGPGSFNRFYQAFAGPHLAANPQTDRDGHVLSSQSTGSSNTEFSVDYLALICGFG  457
             : :|  .:. :||:|.:|   .::||:||  :| :  |||| :| :||:::|  ||.:
Db  344 RIAVRGGADRFDIVETRHGPVIAGDP---LEGAALTLRSVQFAETDLSFDCLTRMP--G   398

Qy  458 APLLARLLFVLERCDAGAFTG--GH---GDALKYVTGTFDSEIPCSLCEKHTRPVCAHT   511
          |.|  ::. :              |:     ::||::|  ||.||.||
Db  399 ASTVAQLY-----DATRGWGLIDHNLVAGDVAGSIGHLVRARVPSRPRENGWLPVPGWS   452

Qy  512 TVHRLR-----QRMPRFGQATRQPIGVFGTMNSQY-----------SDCDPLGNYAPY---  553
            | ::     |.||: |.::|:  ::  :.  :|           :||  |.||
Db  453 GEHEWRGWIPHEAMPR---VIDPPGGLIVTANNRVVADDHPDYLCTDCHP-----PYRAE   504

Qy  554 ----LILRKPGDQTEAAKATMQDT------YRATLERLFI--DLEQERL----------  590
            :|:||  | :  :||:|  ||:    :||.||: |:  |||:||
Db  505 RIMERLVASPAFAVDDAAAIHADTLSPHVGLLRARLEALGIQGSLPAEELRQTLIAWDGR  564

Qy  591 LDRGAPCSSEGLSSVIVDHPTFRRILDTLRARIEQTTTQFMKVLVETRDYKIREGLSEA-  649
          :|: :.:                     |:|||:|           ||:||||| ||:||
Db  565 MDAGSQAASA---------YNAFRRAL-----------------TRLVTARSGLEQAI    596

Qy  650 THSMALT---FDPYSGAFCPITNFLVKRTHLAVVQ----DLALSQCHCVFYGQQVEGRNF  702
            ::: |:   |||:||.|||||:|.|:|||:|:|      :::.   |.:   .:::|.|
Db  597 AHPFAAVPPGVSPQGQVWWAVPT-LLRNDDAGMLKGWSWDEALSEALSV-ATQNLTGRGW  654

Qy  703 RNQFQPVLRRRFVDLFNGGFISTRSITVTLSEGPVSAP------------NPTLGQDAP  749
            ::.: :  .| :. |.|.:  :    :  || |||:|            |||:.| |||
Db  655 GEEHRP---RFTHPLSAQFPAWAALL-----NPVSRPIGGDGDTVLANGLVPSAGPEAT  705

Qy  750 AGRTFDGDLARVSVEVIRDIRVKNRVVFS-GNCTNLSEAARARLVGLASAVQRQEKRVDM  808
           || ::.| | |::    .|:                 || :::|:.|  |.|
Db  706 YG----------------------ALSRYVFDVGNWDN-------------------   726

Qy  809 LHGALGFLLKQFHGLLFPRGMPPNSKSPNPQW-----FWTLLQRNQMPADKLTHEEI   860
            |:|| .|| |:|   .|.|.|         |
Db  727 FHGASG---------HPASPHYADQNAPWSDCAMVPMLYSWDRIAAEAVTSQEL     771
```

```
Db 1732 VLEPLSRAR---ANG-----HQVLAVLRGSAVNQDGASNGLAAPNGPSQERVIRQALAA 1782
          .:|| .| |     ::|:   |  ||.|.||:|:|           .:|||:|.:.  ||
Qy  761 VSVEVIRDIRVKNRVVFSSGNCTNLSEAARARLVGLASAYQRQEKR------VDMLH-- 810
Db 1783 SGVPA-ADVDV--VEAHGTGTELGDPIEAG--ALIATYGQDRDPLRLGSVKTNIGHTQ 1836
          ||||. ||.:     :|:|:|.|||.:|:.    ||:||:| || |:||.| .|.:||:|
Qy  811 ------GALGFLLKQPHGLLFPRGMPPNSKSPNPQWFWTLLQRNQMPADKLTHEITTIA 864
Db 1837 AAAGAAGVIKVVLAMRHGML-PRSLHADELSPHIDW--------ESGAVEVLREEVPWPA 1887
          |:|.|.|:|:||||||:|| .||||.|||||||:||        ||||.|.|:|||.||.|
Qy  865 AVKRFTEEYAAINFINLPPTCIGELAQFYMANLLILKYCDHSQYLINTLTSIITGARRPRD 924
Db 1888 GER---PRRAGVSSFGVSGT--------NAHVIVEEAPAEQ----------EAARTERG 1925
          |:.   |:.|||||||||:|        ||||.|:||||||          |||||:||:|
Qy  925 PSSVLHWIRKDVTSAADIETQAKALLEKTENLPEL------WTTAFTSTHL-VRAAMNQR 977
Db 1926 PLPFVLSGRSEAVVAA---QARALAEHLRDTPELGLTDAAWTLATGRARFDVRAAV---- 1978
          |.|.||:.| .|.:||   .||||||||||||||||||||| |.|.||||.||||||.  
Qy  978 PMVVLGISISKYHGRAAGNNRVFQAGNWSGLNGGKNVCPLFTFDRTRRFIIACPRGGFICP 1037
Db 1979 --------LGDDRAGVCAELDALAEGR-------------PSADAVAP 2005
          :.||:|||||||||||||||||||||||||:||||       |||||||
Qy 1038 VTGPSSGNRETTLSDQVRGIIVSGGAMVQLAIYATVVRAVGARAQHMAFDDWLSLTDDEF 1097
Db 2006 VT---SAPRKPVL------------------VFPGGQAQ------WVG------ 2026
          |:   ||||||||:                  ||||||||      ||:|
Qy 1098 LARDLELHDQIQTL----------ETPWTVEGALEAVKILDEKTTAGDG 1138
Db 2027 MARDLLESSEVPAESMSRCAEALSPHIDW-------KLLD--VVRGDG 2065
          :||||||.||:|:|||||||||||||||||       :|||  ||||||
```

RESULT 15
US-07-731-157A-7
; Sequence 7, Application US/07731157A
; Patent No. 5457032
GENERAL INFORMATION:
  APPLICANT: Quax, Wilhelmus J.
  APPLICANT: Misset, Onno
  APPLICANT: Van der Laan, Jan M.
  APPLICANT: Lenting, Herman B.M.
  TITLE OF INVENTION: Mutated beta-lactam acylase genes
  NUMBER OF SEQUENCES: 50
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: COOLEY GODWARD CASTRO HUDDLESON & TATUM
    STREET: FIVE PALO ALTO SQUARE, 4TH FLOOR
    CITY: PALO ALTO
    STATE: CALIFORNIA
    COUNTRY: USA
    ZIP: 94306
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/07/731,157A
    FILING DATE: 19910509
    CLASSIFICATION: 435
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: EP 90200962
    FILING DATE: 18-APR-1990
  ATTORNEY/AGENT INFORMATION:
    NAME: RAE-VENTER PH.D., BARBARA
    REGISTRATION NUMBER: 32,750
    REFERENCE/DOCKET NUMBER: GBRO-027/00US
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: 415-494-7622
    TELEFAX: 415-857-0663
    TELEX: 380816 COOLEY PA
  INFORMATION FOR SEQ ID NO: 7:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 774 amino acids

RESULT 16
US-08-541-780-7
; Sequence 7, Application US/08541780
; Patent No. 5935831
GENERAL INFORMATION:
  APPLICANT: Quax, Wilhelmus J.
  APPLICANT: Misset, Onno
  APPLICANT: Van der Laan, Jan M.
  APPLICANT: Lenting, Herman B.M.
  TITLE OF INVENTION: Mutated beta-lactam acylase genes
  NUMBER OF SEQUENCES: 50

```
CORRESPONDENCE ADDRESS:
    ADDRESSEE: COOLEY GODWARD CASTRO HUDDLESON & TATUM
    STREET: FIVE PALO ALTO SQUARE, 4TH FLOOR
    CITY: PALO ALTO
    STATE: CALIFORNIA
    COUNTRY: USA
    ZIP: 94306
COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/541,780
    FILING DATE:
    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US/07/731,157
    FILING DATE:
    APPLICATION NUMBER: EP 90200962
    FILING DATE: 18-APR-1990
ATTORNEY/AGENT INFORMATION:
    NAME: RAE-VENTER PH.D., BARBARA
    REGISTRATION NUMBER: 32,750
    REFERENCE/DOCKET NUMBER: GBRO-027/00US
TELECOMMUNICATION INFORMATION:
    TELEPHONE: 415-494-7622
    TELEFAX: 415-857-0663
    TELEX: 380816 COOLEY PA
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
    LENGTH: 774 amino acids
    TYPE: amino acid
    TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
    ORGANISM: Pseudomonas species
    STRAIN: SB3
US-08-541-780-7

Query Match          1.7%;  Score 106; DB 2;  Length 774;
Best Local Similarity   20.2%;  Pred. No. 0.47;
Matches 145;  Conservative 79;  Mismatches 251;  Indels 242;  Gaps 37;

Qy  258 ARGAAHLAFDENHEGAV-LPPDITYTYFQSSSSGTTTARGARRNDVNSTSKPSPSGGFER 316
Db  183 AANALKLRYDDGGQDLLCIPPGVEAERLEADLAALRPAVDALLKAMGGDASDAAGGGSNN 242

Qy  317 -----RLAS---IMAADTALHAEVIFNTGIYEETPTDIKEWPMFIGMEGTLPRLNALGS 367
Db  243 WAVAPGRTATGRPILAGDPHRVFEI---PGMYAQHHLACDRFDM-IGL--TVP------ 289

Qy  368 YTARVAGVIGAMVFSPNSA----------------LYLTEVEDSGMTE--------- 399
Db  290 ------GVPGFPHFAHNGKVAYCVTHAFMDIHDYLEQFAEDGRTARFGNEFEPVAWRRD 343

Qy  400 --AKDGGPGSFNRFYQFAGPHLAANPQTDRDGHVLSSQSTGSSNTEFSVDYLALICGFG 457
Db  344 RIAVRGGADREFDIVETRHGPVIAGDP---LEGAALTLRSVQFAETDLSFDCLTRMP--G 398

Qy  458 APLLARLLFYLERCDAGAFTG--GH----GDALKVTGTPDSEIPCSLCEKHTRPVCAHT 511
Db  399 ASTVAQLY------DATRGWGLIDHNLVAGDVAGSIGHLVRARVPSRPENGWLPVPGWS 452

Qy  512 TVHRLR------QRMPRFGQATRQPIGVFGTMNSQY----------SDCDPLGNYAPY--- 553
Db  453 GEHEWRGWIPHEAMPR---VIDPPGGLIVTANRRVVADDHPDYLCTDCHP-----PYRAE 504

Qy  554 ---LILRKPGDQTEAAKATMQDT----YRATLERLFI-DLEQERL---------- 590
Db  505 RIMERLVASPAFAVDDAAAIHADTLSPHVGLLRARLEALGIQGSLPAEELRQTLIAWDGR 564
```

```
Qy  591 LDRGAPCSSEGLSSVIVDHPTFPRRILDTLRARIEQTTTQFMKVLVETRDYKIREGLSEA- 649
                                                      TRLVTARSGLEQAI 596
Db  565 MDAGSQAASA--------YNAFRRAL----------

Qy  650 THSMALT---FPDYSGAFCPITNFLVKRTHLAVVQ---DLALSQCHCVFYGQQVEGRNF 702
Db  597 AHFFAAVPPGVSPQGQVWWAVPT-LLRNDDAGMLKGWSWDEALSEALSV-ATQNLTGRGW 654

Qy  703 RNQFQPVLRRRFVDLFNGGFISTRSRIVTLSEGPVSAP------------NPTLGQDAP 749
Db  655 GEEHRP---RFTHPLSAQFFAWAALL-----NPVSRPIGGDGDTVLANGLVPSAGPEAT 705

Qy  750 AGRTFDGDLARVSVEVIRDIRVKNRVVFS-GNCTNLSEAARARLVGLLASAYQRQEKRVDM 808
Db  706 YG---------------------ALSRYVFDVGNWDN----------SRVVV 726

Qy  809 LHGALGFLLKQFHGLLFPRGMPPNSKSPNPQW-----FWTLLQRNQMPADKLTHEEI 860
Db  727 FHGASG----------HPASPHYADQNAPWSDCAVVPMLYSWDRIAAEAVTSQEL 771


RESULT 17
US-09-107-532A-3855
; Sequence 3855, Application US/09107532A
; Patent No. 6581275
GENERAL INFORMATION:
    APPLICANT: Lynn A Doucette-Stamm  and David Bush
    TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
                        ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
    ADDRESSEE: GENOME THERAPEUTICS CORPORATION
    STREET: 100 Beaver Street
    CITY: Waltham
    STATE: Massachusetts
    COUNTRY: USA
    ZIP: 02354
COMPUTER READABLE FORM:
    MEDIUM TYPE: CD/ROM ISO9660
    COMPUTER: PC
    OPERATING SYSTEM: <Unknown>
    SOFTWARE: ASCII
CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/107,532A
    FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 60/085,598
    FILING DATE: 14 May 1998
    APPLICATION NUMBER: 60/051571
    FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
    NAME: Ariniello, Pamela Deneke
    REGISTRATION NUMBER: 40,489
    REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
    TELEPHONE: (781)893-5007
    TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 3855:
SEQUENCE CHARACTERISTICS:
    LENGTH: 1095 amino acids
    TYPE: amino acid
    TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
    ORGANISM: Enterococcus faecium
FEATURE:
    NAME/KEY: misc feature
    LOCATION: (B) LOCATION 1...1095
SEQUENCE DESCRIPTION: SEQ ID NO: 3855:
US-09-107-532A-3855

Query Match          1.7%;  Score 105.5;  DB 4;  Length 1095;
```

STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/633,760
  FILING DATE: 01-MAY-1996
  CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
  NAME: OBLON, NORMAN F.
  REGISTRATION NUMBER: 24,618
  REFERENCE/DOCKET NUMBER: 18-929-0 PCT
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (703) 413-3000
  TELEFAX: (703) 413-2220
  TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 46:
  SEQUENCE CHARACTERISTICS:
  LENGTH: 774 amino acids
  TYPE: amino acid
  TOPOLOGY: linear
  MOLECULE TYPE: protein
US-08-633-760-46

Query Match   1.7%; Score 105; DB 1; Length 774;
Best Local Similarity 20.7%; Pred. No. 0.6;
Matches 146; Conservative 76; Mismatches 241; Indels 242; Gaps 37;

Qy 109 LTR--ACNAARERFGFSRCQGPPVDGAVETTGAE-ICTR----LGLEPENTILYLVVTAL 161
Db   70 LTRRKALGRAAEWLG--ABAAEADILVRRLGMEKVCRRDFEALGVEAKD-----------M 117

Qy 162 FKEAVFMCNVFLHYGGLDIVHINHGDVIRIPLFPVQLFMPDVNRLVPDPNTHH----R 216
Db 118 LRAYVAGVNAFLASGA-------------PL-PVEYGLLGAE--PEPWEPWHSIAVMR 159

Qy 217 SIGEGFVYPTPFYNTGLCHLIHDCVIAPMAVALRVRNVIAV---ARGAAHLAPDENHEG 272
Db 160 RLG--------------------LLMGAVWFKLWRMLALPVVGAANALXLRYDDGGRD 197

Qy 273 AV-LPPDITYTYFQSSSSGTTTARGARRNDVNSTSKPSPSGGFER------RLAS--IM 322
Db 198 LLCIPPGAEADRLEADLATLRPAVDALLKAMGGDASDAAGGGSNNWAVAPGRTATGRPIL 257

Qy 323 AADTALHABVIFNTGIYEETPTDIKEWPMFIGMEGTLPRLNALGSYTARVAGVIGAMVFS 382
Db 258 AGDPHRVFEI---PGMYAQHLLACDRFDM-IGL---TVP--------------GVPGPHFA 298

Qy 383 PNSA---------------LYLTEVEDSGMTE-------------AKDGGGPGPSFNRF 412
Db 299 HNGKVAYCVTHAFMDIHDLYLEQFAGEGRTARFGNDFEPVAWSRDRIAVRGGADRBFDIV 358

Qy 413 YQFAGPHLAANPQTDRDGHVLSSQSTGSSNTEFSVDYLALICGFGAPLLARLLFYLERCD 472
Db 359 ETRHGPVIAGDP---RDGAALTLRSVQFAETDLSFDCLTRMP--GASTVAQLY------D 407

Qy 473 AGAFTG--GH----GDALKVTGTFDSEIPCSLCEKHTRPVCAHTTVHRLR-----QRMP 521
Db 408 ATRGWGLIDHNLVAGDVAGSIGHLVRARVPSRPRRNGWLPVPGWSGEHEWRGWIPHEAMP 467

Qy 522 RFGQATRQPIGVFGTMNSQY--------SDCDPLGNYAPY-------LILRKPGDQTE 564
Db 468 R---VIDPPGGIIVTANNRVVADDHPDYLCTDCHP-----PYRAERIMKRLVANPAFAVD 519

Qy 565 AAKATMQDTYRATLERLFIDLEQERLLDRGA--PCSSEGLSSVIV----------D 608
Db 520 DAAAIHADTLSP-----HVGLLRRRLEALGARDDSAAEGLRQMLVAWDGRMDAASEVASA 574

Qy 609 HPTFRRILDTL--RARIEQTTTQ-----------------FMKVLVETRDYKIREG--- 645

Best Local Similarity 18.9%; Pred. No. 1;
Matches 145; Conservative 112; Mismatches 298; Indels 211; Gaps 35;

Qy 551 APYLLLRKPGDQTEAAKATMQDTYRATLERLFIDLEQERLLDRGAPCSSEGLS-----S 604
Db 360 APYTIDTTPMTTIKAGETIVTSKNAQEKGQIILDKSG-VETGSDLWNDNYSLAGNTFA 418

Qy 605 VIVDHPTFRRILD-TLRARIEQTTTQFMKVLVETRDYKIREGLSRATHSMALTFDD---- 659
Db 419 IRKDSPTGEIVQEMTDENGHAETPKEIANALELGTYYVTE--TKASHGFVNTFKPVKVE 476

Qy 660 --YSGAPCPITNFLVKRTHLAVVQDLAL----------SQCHCVFYGGQV------EGR- 700
Db 477 LKYANQTVALVTSNVKGQNQEVTGETTLTKEDKDTGDKAQGKAVFEGTEYTLFTAKDGKA 536

Qy 701 -NFRNQFQPVLRRRFVDLFNGGFISTRSIITVTLSEGPVSAP-----NPTLGQD--APAGR 752
Db 537 VKWSEAFKP------EMVKGTKASDETVTLALDEKNQAAVKHLAINEYTWQSTKAPEGY 589

Qy 753 TFDGDLARVSVE------------VIRDIRVKNRVV---------FSGNCTNLSEAA------ 788
Db 590 TLDETKYPVSIKKVDDNEKNAVITRDVTAKEQIIRFGFDFFKPAGSAAGTAETGFNDLTF 649

Qy 789 -RARLVGLASAVQRQEKRVDMLHGALGF-------------LLKQFHGLLFPRGM----- 829
Db 650 KVSPLEGTNEITGAEDEATTAYNEQLGFDGVGKFENLPYGDYLLEEVEA---PEGFQKIT 706

Qy 830 PPNSKSP-----------NPQWFWTLLQRNQ------MPADKLTHEEITTIAAVKRFTEE 872
Db 707 PLEIRSTFKENKEDFVKSEYVFTITEQDQKQPIKTVTVPYEKLTN---------KAFSVS 757

Qy 873 YAAINFINLP--PTCIGELAQFYMANLILKYCDHSQYLINTLTSIITGARRPRDPSSVLH 930
Db 758 LNRLMLYDLPEEEDSLTSLATWKDGNKELTSLDSTE-LVDKL-----------SYNLH 803

Qy 931 WIRKD---VTSAADIETQAKALLEKTENLPELWTAFTSTHLVRAAMN----QRPMV-- 980
Db 804 EIKEDWTVVAQAIDVDA-TKAAQEKDEKAKPV-VIAETSATLANKEKTGTWKIQHLTAE 861

Qy 981 -VLGISISKYHGAAGNNRVFQAGNWSGLNGGKNVCPLFTFDRTRRFIIACPRGGFICPVT 1039
Db 862 QVLNKTIVLFNYVYENKEAFEAGD--------------------------KPVA 889

Qy 1040 GPSSGNRETTLSDQVRGIIVSGGAMVQLAIYATVVRAVGARAQHMAFDDWLSLTDDEFLA 1099
Db   890 ---KDVSLNNQAQTVSCTVEHHVSIQTKAHLENG----SQTFTHGDVVDMFDDVSIT 939

Qy 1100 RDL-----BELHDQIIQTLETPWTVEGALEAVKILDE------KTT----AGDGETPTNL 1144
Db   940 HDVLDGSKEAFETILYALLPDGTNKEIWKSGKIEYEVNDKEFTKTVLAKKVDTGKYPEGT 999

Qy 1145 AFNFDSCEPSHDTTSN-----VLNISSSNISGSTVPGLKRPPEDDE 1185
Db 1000 KFTFAEINYDKDGTINGKHNEDLKEKSQTLTPKEVFPILSTPKQPE 1045

RESULT 18
US-08-633-760-46
; Sequence 46, Application US/08633760
Patent No. 5804429
GENERAL INFORMATION:
  APPLICANT: NIWA, MINEO
  APPLICANT: SAITO, YOSHINASA
  APPLICANT: FUJIMURA, TAKAO
  APPLICANT: ISHII, YOSHINORI
  APPLICANT: NOGUCHI, YUJI
  TITLE OF INVENTION: A NEW CEPHALOSPORIN C ACYLASE
  NUMBER OF SEQUENCES: 64
  CORRESPONDENCE ADDRESS:
  ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
  ADDRESSEE: P.C.
  STREET: 1755 JEFFERSON DAVIS HIGHWAY, SUITE 400
  CITY: ARLINGTON

Qy   323 AADTALHAEVIFNTGIYEETPTDIKEWPMFIGMEGTLPRLNALGSYTARVAGVIGAMVFS 382
                 |: |: |: |: ||
Db   258 AGDPHRVPEI---PGIYAQHHLACDRFDM-IGL--TVP-----------------GVPGFPHFA 298

Qy   383 PNSA---------------------LYLTEVEDSGMTE------------------AKDGGPGPSFNRF 412
                 ||| |||
Db   299 HNGKVAYCVTHAFMDIHDLYLEQFAGEGRTARFGNDFEPVAWSRDRIAVRGGADREFDIV 358

Qy   413 YQPAGPHLAANPQTDRDGHVLSSQSTGSSNTEPSVDYLALICGFGAPLLARLLFYLERCD 472
                 |:|:|| :|: | :|:|| :|: ||: |: |:|: :|:
Db   359 KTRHGPVIAGDP---RDGAALTLRSVQPAETDLSFDCLTRMP--GASTVAQLY-------D 407

Qy   473 AGAFTG--GH----GDALKYVTGFDSEIPCSLCEKHTRPVCAHTTVHRLR-----QRMP 521
                 |:   :|::||:   : | |: ||: |
Db   408 ATRGWGLIDHNLVAGDVAGSIGHLVRARVPSRPRENGWLPVPGWSGEHEWRGWIPHEAMP 467

Qy   522 RFGQATRQPIGVFGTMNSQY--------------SDCDPLGNYAPY----------LILRKPGDQTE 564
                 | :|::   :||
Db   468 R---VIDPPGGIIVTANNRVVADDHPDYLCTDCHP------PYRAERIMKRLVANPAFAVD 519

Qy   565 AAKATMQDTYRATLERLFIDLEQERILLDRGA--PCSSEGLSSVIV-----------D 608
                 | : || ||: |: :|| :|||: :|:
Db   520 DAAIHADTLSP-----HVGLLRRRLALGARDDSAAEGLRQMLVAWDGRMDAASEVASA 574

Qy   609 HPTFRRILDTL---RARIEQTTQ------------------FMKVLVETRDYKIREG---- 645
                 : |:|| |:|:|| ||:   :
Db   575 YNAFRRALTRLVTDRSGLEQAISHPFAAVAPGVSPGQVWWAVPTLLRDDDAGMLKGWSW 634

Qy   646 ---LSEA-----------------THSMALTFDPYSGAFCP 666
                 |||| |: |:
Db   635 DQALSEALSVASQNLTGRSWGEEHRPRFTHPLATQFPAWAGLLNP 679

RESULT 20
US-08-931-608A-5
; Sequence 5, Application US/08931608A
; Patent No. 6302685
; GENERAL INFORMATION:
; APPLICANT: Lobel, Peter
; APPLICANT: Sleat, David E.
; TITLE OF INVENTION: NOVEL HUMAN LYSOSOMAL PROTEIN AND METHODS OF ITS USE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: David A. Jackson, Esq.
;   STREET: 411 Hackensack Ave, Continental Plaza, 4th Floor
;   CITY: Hackensack
;   STATE: New Jersey
;   COUNTRY: USA
;   ZIP: 07601
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/931,608A
;   FILING DATE:
;   CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
;   NAME: Jackson Esq., David A.
;   REGISTRATION NUMBER: 26,742
;   REFERENCE/DOCKET NUMBER: 601-1-077
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 201-487-5800
;   TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 635 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO

Db   575 YNAFRRALTRLVTDRSGLEQAISHPFAAVAPGVSPGQVWWAVPTLLRDDDAGMLKGWSW 634
                 |: | | | |:| || ||: |:||
Qy   646 ---LSEA----------------THSMALTFDPYSGAFCP 666
                 |||| |: |:
Db   635 DQALSEALSVASQNLTGRSWGEEHRPRFTHPLATQFPAWAGLLNP 679

RESULT 19
US-08-633-760-48
; Sequence 49, Application US/08633760
; Patent No. 5804429
; GENERAL INFORMATION:
; APPLICANT: NIWA, MINEO
; APPLICANT: SAITO, YOSHIMASA
; APPLICANT: FUJIMURA, TAKAO
; APPLICANT: ISHII, YOSHINORI
; APPLICANT: NOGUCHI, YUJI
; TITLE OF INVENTION: A NEW CEPHALOSPORIN C ACYLASE
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;   ADDRESSEE: P.C.
;   STREET: 1755 JEFFERSON DAVIS HIGHWAY, SUITE 400
;   CITY: ARLINGTON
;   STATE: VIRGINIA
;   COUNTRY: USA
;   ZIP: 22202
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/633,760
;   FILING DATE: 01-MAY-1996
;   CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
;   NAME: OBLON, NORMAN F.
;   REGISTRATION NUMBER: 24,618
;   REFERENCE/DOCKET NUMBER: 18-929-0 PCT
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (703) 413-3000
;   TELEFAX: (703) 413-2220
;   TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 774 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-633-760-48

Query Match   1.7%; Score 105; DB 1; Length 774;
Best Local Similarity 20.7%; Pred.No. 0.6;
Matches 146; Conservative 76; Mismatches 241; Indels 242; Gaps 37;

Qy   109 LTR--ACNAARERFGFSRCCGPPVDGAVETTGAE-ICTR-----LGLEPENTILYLVVTAL 161
                 ||| |: || : |: |:|: :|
Db   70 LTRRKALGRAAEWLG--AEAAEADILVRRLGMEKVCRRDFEALGVEAKD---------M 117

Qy   162 FKEAVFMCNVFLHYGGLDIVHINHGDVIRIPLFPVQLFMPDVNRLVPDPFNTHH-----R 216
                 |:|| | ::| |: |:
Db   118 LRAYVAGVNAFLASGA-------------PL-PVEYGLLGAE--PEPWBPWHSIAVMR 159

Qy   217 SIGEGFVYPTPFYNTGLCHLIHDCVIAPMAVALRVRNVTAV----ARGAAHLAFDENHEG 272
                 :| ||:
Db   160 RLG----------------LLMGSVWFKLWRMLALPVVGAANALKLRYDDGGRD 197

Qy   273 AV-LPPDITYTYFQSSSGTTARGARRNDVNSTSKPSPSGGFER------RLAS---IM 322
                 |:|| | |: ||
Db   198 LLCIPGAZADRLEADLATLRPAVDALLKAMGGDASDAAGGSNNWAVAPGRTATGRPIL 257

US-08-931-608A-5

```
Query Match        1.7%;     Score 104.5;  DB 4;  Length 635;
Best Local Similarity    21.0%;   Pred. No. 0.47;
Matches  77;  Conservative 36;  Mismatches 121;  Indels 133;  Gaps 14;

Qy  245 MAVALRVRNVTAVARGAAHLAFDENH-EGAVLPPDITYTYFQSSSGTTTARGARRNDVN 303
            :||::|..::::|..       ::        |.|::.|
Db   10 VAIALAMSSLSAHAED---AWVSTHTQAMSPPASTQVLAASSTSATTGNA---YTLN 62

Qy  304 STSKPSPSGGFERRLASIMAADTALHAEVIFNTGIYEETPTDIKEWPMFIGMEGTLPRLN 363
                 :       |.|||:  :                                 :
Db   63 MTGSPRIDGA---AVTALEADHPLHVEVALK----------------------LRNPD 95

Qy  364 ALGSYTARVAGVIGAMVFSPNSALYLTEVEDSGMTEAKDGGPGPSFNRFYQFAGPHLAAN 423
            ||:|: :       :|||                       :      RF----GP-----
Db   96 ALQTFLAGVT--------TPGSALFGKFLTPSQFTE----------RF----GP----- 127

Qy  424 PQTDRDGHVLSSQSTGSSNTEFSVDYLALICGFGAPLLARLLFYLERCDAGAFTGGHGDA 483
            |   :      |      :||:  :  ||:                     AGAATNGFRTS
Db  128 TQSQVDAVVAHLQQAGFTNIEVAPNRL-LISADGT---------------AGAATNGFRTS 172

Qy  484 LKYVTGTFDSEIPCSLCEKHTRPVCAHTTVHRLRQRMPRFGQATRQPIGVFGTMNSQYSD 543
                 :       |||          :::  RFSANGR
Db  173 IK--------------------------RFSANGR------------------------- 181

Qy  544 CDPLGNYAPYLILRKPGDQTEAAKATMQDTYRATLERLFIDLEQERLLDRGAPCSSEGLS 603
            |          :    ||            ::                    :::
Db  182 -EFFANDAPALVPASLGDSVNAVLGLQNVSVKGHTLHHVY---HPEDVTVPGPNVGTQAAA 237

Qy  604 SVIVDHP 610
            :||
Db  238 AVAAHHP 244
```

RESULT 21
US-09-851-847-5
; Sequence 5, Application US/09851847
; Patent No. 6638712
; GENERAL INFORMATION:
;   APPLICANT: Lobel, Peter
;   Sleat, David E.
;   TITLE OF INVENTION: NOVEL HUMAN LYSOSOMAL PROTEIN AND METHODS OF ITS USE
;   NUMBER OF SEQUENCES: 12
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: David A. Jackson, Esq.
;   STREET: 411 Hackensack Ave, Continental Plaza, 4th Floor
;   CITY: Hackensack
;   STATE: New Jersey
;   COUNTRY: USA
;   ZIP: 07601
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/851,847
;   FILING DATE: 09-May-2001
;   CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/931,608
;   FILING DATE: <Unknown>
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Jackson Esq., David A.
;   REGISTRATION NUMBER: 26,742
;   REFERENCE/DOCKET NUMBER: 601-1-077
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 201-487-5800
;   TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 5:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 635 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   HYPOTHETICAL: NO
;   SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-851-847-5

```
Query Match        1.7%;     Score 104.5;  DB 4;  Length 635;
Best Local Similarity    21.0%;   Pred. No. 0.47;
Matches  77;  Conservative 36;  Mismatches 121;  Indels 133;  Gaps 14;

Qy  245 MAVALRVRNVTAVARGAAHLAFDENH-EGAVLPPDITYTYFQSSSGTTTARGARRNDVN 303
            :||::|..::::|..       ::        |.|::.|
Db   10 VAIALAMSSLSAHAED---AWVSTHTQAMSPPASTQVLAASSTSATTGNA---YTLN 62

Qy  304 STSKPSPSGGFERRLASIMAADTALHAEVIFNTGIYEETPTDIKEWPMFIGMEGTLPRLN 363
                 :       |.|||:  :                                 :
Db   63 MTGSPRIDGA---AVTALEADHPLHVEVALK----------------------LRNPD 95

Qy  364 ALGSYTARVAGVIGAMVFSPNSALYLTEVEDSGMTEAKDGGPGPSFNRFYQFAGPHLAAN 423
            ||:|: :       :|||                       :      RF----GP-----
Db   96 ALQTFLAGVT--------TPGSALFGKFLTPSQFTE----------RF----GP----- 127

Qy  424 PQTDRDGHVLSSQSTGSSNTEFSVDYLALICGFGAPLLARLLFYLERCDAGAFTGGHGDA 483
            |   :      |      :||:  :  ||:                     AGAATNGFRTS
Db  128 TQSQVDAVVAHLQQAGFTNIEVAPNRL-LISADGT---------------AGAATNGFRTS 172

Qy  484 LKYVTGTFDSEIPCSLCEKHTRPVCAHTTVHRLRQRMPRFGQATRQPIGVFGTMNSQYSD 543
                 :       |||          :::  RFSANGR
Db  173 IK--------------------------RFSANGR------------------------- 181

Qy  544 CDPLGNYAPYLILRKPGDQTEAAKATMQDTYRATLERLFIDLEQERLLDRGAPCSSEGLS 603
            |          :    ||            ::                    :::
Db  182 -EFFANDAPALVPASLGDSVNAVLGLQNVSVKGHTLHHVY---HPEDVTVPGPNVGTQAAA 237

Qy  604 SVIVDHP 610
            :||
Db  238 AVAAHHP 244
```

RESULT 22
US-08-019-870-5
; Sequence 5, Application US/08019870
; Patent No. 536613
; GENERAL INFORMATION:
;   APPLICANT: NIWA, MINEO
;   APPLICANT: YOSHIMASA, SAITO
;   APPLICANT: SASAKI, HITOSHI
;   APPLICANT: ISHII, YOSHINORI
;   TITLE OF INVENTION: A NEW CEPHALOSPORIN C ACYLASE
;   NUMBER OF SEQUENCES: 42
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
;   ADDRESSEE: P.C.
;   STREET: 1755 S. Jefferson Davis Highway, Suite 400
;   CITY: Arlington
;   STATE: Virginia
;   COUNTRY: U.S.A.
;   ZIP: 22202
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/019,870
;   FILING DATE: 19930219
;   CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Oblon, No. 535613man F.
;   REGISTRATION NUMBER: 24,618

```
    REFERENCE/DOCKET NUMBER: 18-791-0
    TELECOMMUNICATION INFORMATION:
    TELEPHONE:  (703) 413-3000
    TELEFAX:    (703) 413-2220
    TELEX:      248855 OPAT UR
    INFORMATION FOR SEQ ID NO:  5:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 774 amino acids
      TYPE: amino acid
      TOPOLOGY: linear
      MOLECULE TYPE: protein
US-08-019-870-5
```

```
Query Match        1.7%;   Score 104.5;  DB 1;   Length 774;
Best Local Similarity  21.7%;  Pred. No. 0.68;
Matches   91;   Conservative  41;  Mismatches  136;  Indels  151;  Gaps   19;

Qy   372  VAGVIGAMVFSPNSA---------------LYLTEVEDSGMTE----------------AK 401
                :| |||                            :|||||:|
Db   288  VPGVVPGFPHFAHNGKVAYCVTHAFMDIHDLYLEQPAGEGRTARFGNDFEPVANSRDRIAV 347

Qy   402  DGGPGPSFNRFYQFAGPHLAANPQTDRDGHVLSSQSTGSSNTEFSVDYLA---------LI 453
                :| :|||:           || : ||:||::||||:|:||:||:|        ||
Db   348  RGGADRFDIVETRHGPVIAGDP---RDGAALTLRSVQFAETDLSFDCLTRMPGASHNIV 404

Qy   454  CGFGAPLLARLLFYLERCDAGAFTGGHGDALKYVTGTFD-SEIPCSLCEKHTRPVCAHTT 512
                ||:||||||||||||||||||||||||||          :||||||||||||||
Db   405  AGDVAGSIGHLVTVAQLYDA---TRG--------WGLIDRARVPSRPRENGWLPVPGWSG 453

Qy   513  VHRLR-----QRMPRPGQATRQPIGVFGTMNSQY----------SDCDPLGNYAPY---- 553
                :|              |:||||||||:||           :||:|||||||
Db   454  EHEWRGWIPHEAMPR---VIDPPGGIIVTANNRVVADDHPDYLCTDCHP----PYRAER 505

Qy   554  ---LILRKPGDQTEAAKATMQDTYRATLERLFIDLEQERILDRGA--PCSSEGLSSVIV- 607
                :||:||      |||||::||||||:|||||||||||||||||:  |::|||:||:||:
Db   506  IMKRLVANPAFAVDDAAAIHADTLSP----HVGLLRRRLEALGARDDSAAEGLRQMLVA 560

Qy   608  ------------DHPTFRRILDTL--RARIEQTTQ------------------FMKVL 634
                            |||:||||||:|  ||:||:||:
Db   561  WDGRMDAASEVASAYNAFRRALTRLVTDRSGLEQAISHPFAAVAPGVSPQGQVWWAVPTL 620

Qy   635  VETRDYKIREG------LSEA----------------THSMALITFDPYSGAFCP 666
                :  :|: |:         ||:|                  ::| |::||||||||:
Db   621  LRDDDAGMLKGWSWDQALSEALSVASQNLITGRSWGEHRPFTHPLATQFPAWAGLLNP 679

RESULT 23
US-08-811-519-1
; Sequence 1, Application US/08811519B
; Patent No. 6630345
; GENERAL INFORMATION:
;   APPLICANT: Petrenko, Alexandre
;   TITLE OF INVENTION: CALCIUM INDEPENDENT RECEPTOR OF ALPHA-LATROTOXIN,
;   TITLE OF INVENTION: CHARACTERIZATION AND USES THEREOF
;   FILE REFERENCE: 1049-1-007
;   CURRENT APPLICATION NUMBER: US/08/811,519B
;   CURRENT FILING DATE: 1997-03-04
;   NUMBER OF SEQ ID NOS: 31
;   SOFTWARE: PatentIn Ver. 2.0
US-08-811-519-1
; SEQ ID NO 1
;   LENGTH: 1471
;   TYPE: PRT
;   ORGANISM: rat
US-08-811-519-1

Query Match        1.7%;   Score 104.5;  DB 4;   Length 1471;
Best Local Similarity  19.6%;  Pred. No. 2.3;
Matches  182;  Conservative   98;  Mismatches  310;  Indels  339;  Gaps   47;

Qy    73  LAGAGITLKLTSHFYPSVFVFHGGKHVLPSSAAPNLTRACNAARERFGFSR----CQGP 128
                ||:||:|:|||||                   :| ||:|:  ::|
Db     4  LAAALWSLCVTT--------------VLVTSATQGLSR----AGLPFGLMRRELACEGY 44
```

```
Qy   129  PVDGAVETTGAEICTRLGLEFENTILYIVTALFKEAVFMCNVFLHYGGLDIVHI---NH 185
                ||:
Db    45  PIB-----------------------------------LRCPGSDVIMVENANY 63

Qy   186  G-----DVIRIPLFPVQLFMPDVNLIVPDPFNTHHRSI---GEGFVYPTPFYNTGLC 234
                |                       :|||: |:||    :|| ::  |::|||||:
Db    64  GRTDDKICDADFPQMENVQCYLPDAFKIMSQRCNNRTQCVVVAGSDAFPDPCPGTYKYL- 122

Qy   235  HLIHDCVIAPMAVALRVRNVTAVARGAAHLAFD--------ENHEGA-----------V 274
                :| :||:
Db   123  EVQYDC-----VPYKVEQKVFVCPGTIQKVLEPTSTHESEHQSGAWCKDPLQAGDRIYV 176

Qy   275  LP--PDITYTYFQSSS-------SGTTTARGARRNDVNSTSKPSPSGGF---------E 315
                ::                  || :|: ||:|      :
Db   177  MPWIPYRTDTLTEYASWEDYVAARHTTTYRLPNRVD-------GTGFVVYDGAVFYNK 227

Qy   316  RRLASIMAADTALH--AEVIFNTGIYEET-----------PTDIK--EWPMFIGMEGT 358
                 ::|                                       |||::
Db   228  ERTRNIVKYDLRTRIKSGETVINTANYHDTSPYRWGGKTDIDLAVDENGLWVIY-ATEGN 286

Qy   359  LPRL-NALGSYTARVAG-------------------VIGAMVFSPNSALYLTEVED 394
                |||:                                :| |||:|::
Db   287  NGRLVVSQLNPYTLRFEGTWETGYDKRSASNAFMVCGVLYLVLRSVYVDDDSEAAGNRVDY 346

Qy   395  SGMTEAKDGGP--------------GPSFNRFY------QFAGPHLAANPQ 425
                ::|                     || |||:
Db   347  APFNTNANREEPVSLAFPNPYQFVSSVDYNPRDNQLYVWNNYFVVRYSLEFGPPDPSAGPA 406

Qy   426  TDRDGHVLSSQSTGSSNTEFSVDYLALICGF-GAPLLARLLFYLERCDAGAFTGGHGDAL 484
                :||                                  :||||||||||||||||||
Db   407  TSPP--LSTTTARPTPLTSTASPAATTPLRRAPLTTHPVGAINQL-----------GPDL 454

Qy   485  KYVTGTFDSEIPCSLCEKHTRP-VCAHTTVHRLRQRMPRFGQATRQP--------------- 530
                ||                    ::|
Db   455  PPATAPASTRRPAPNLHVSPELFCEPREVRRVQWPATQQGMLVERPCPKGTRGIASFQ 514

Qy   531  ----IGVFGTMNSQYSDC-DPLGNYAPYLILRKPGDQ----TEAAKATMQDTYRATLER 580
                     |
Db   515  CLPALGLMNPRGPDLSNCTSPWVNQVAQKI---KSGENAANIASELARHT--------- 561

Qy   581  LFIDLEQERLLDRGAPCSSEGLSSVIVDHPTFRRILDTLRARI--------------- 623
                ::
Db   562  ----------RGSIYAGDVSSSV-----KLMEQLLDILDAQLQALRPIBRESAGKNYNK 605

Qy   624  ----EQTTTQFMKVLVETRDYKIR-EGL----------SEATHSMALITFDPY-SGAFCPITN 665
                 ::
Db   606  MHKRERTCKDYIKAVVETVDNLLRPEALESWKDMNATEQVHTATMLLDVLEEGAFLLADN 665

Qy   670  -------FLVKRTHLAV-------------VQDLALSQCHCVFYGQQVEGRNFR-NQFQPVLRR 712
                ||:                ||:
Db   666  VREPARFLAAKQNVVLEVTVLSTEGGVQELVFPQBYASESSIQUSANTIKQNSRNGVKV 725

Qy   713  RFVDLPN--GGFISTRSITVTL----SEGPVSAPNPTLGQ------DAPAGRTFDGDLA 759
                :||:| :|:||  :|                  ||:|||||
Db   726  VFI-LYNNLGLFLSTENATVKLAGAGTGPGGASLVVNSQVIAASINKSSRVF---LM 781

Qy   760  RVSVEVIRDIRVKNRVVFSGNCT-NLSE 786
                ::|
Db   782  DPVIFTVAHLEAKNH--FNANCSFWNYSE 808
```

```
RESULT 24
US-08-019-870-3
; Sequence 3, Application US/08019870
; Patent No. 5336613
; GENERAL INFORMATION:
;   APPLICANT: NIWA, MINEO
;   APPLICANT: YOSHIMASA, SAITO
;   APPLICANT: SASAKI, HITOSHI
;   APPLICANT: ISHII, YOSHINORI
;   TITLE OF INVENTION: A NEW CEPHALOSPORIN C ACYLASE
;   NUMBER OF SEQUENCES: 42
;   CORRESPONDENCE ADDRESS:
```

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/019,870
FILING DATE: 19930219
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5335613man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-791-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
SEQUENCE CHARACTERISTICS:
LENGTH: 435
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
INFORMATION FOR SEQ ID NO: 3:
US-08-019-870-3

```
Query Match                1.6%;   Score 103;   DB 1;   Length 774;
Best Local Similarity    20.5%;    Pred. No. 0.97;
Matches  143;  Conservative  80;  Mismatches 248;  Indels 226;  Gaps  37;

Qy  109  LTR--ACNAARERFGFSRCQGPPVDGAVETTGAE-ICTR----LGLEPENTILYLVVTAL 161
Db   70  LTRRKALGRAAEWLG--AEAAEADILVRRLGMEKVCRRDFEALGVEAKD--------M 117

Qy  162  FKEAVFMCNVFLHYGGLDIVHINHGDVIRIPLFPVQLFMPDVNRLVPDPFNTHH----R 216
Db  118  LRAYVAGVNAFLASGA-------------PL-PVEYGLLGAE---PEPWEPWHSIAVMR 159

Qy  217  SIGEGFVYPTPFYNTGLCHLIHDCVIAPMAVALRVRNVTAV-----ARGAAHLAFDENHEG 272
Db  160  RLG----------------LLMGSVWFKLWRMLALPVVGAANALKLRYDDGGRD 197

Qy  273  AV-LPPDITYTYFQSSSSGTTARGARRNDVNSTSKPSPSGGFER------RLAS---IM 322
Db  198  LLCIPPGAERDRLEADLIATLRPAVDALLKAMGGDASDAAGGGSNNWAVAPGRTATGRPIL 257

Qy  323  AADTALHAEVIFNTGIYEETTDIKEWPMFIGMEGTLPRLNALGSYTARVAGVIGAMVFS 382
Db  258  AGDPHRVFEI---PGMYAQHHLACDRFDM-IGL--TVPGVPGFPHFAHN-----GKVAYS 306

Qy  383  PNSA------LYLTEVEDSGMTE---------AKDGGPGPSFNRFYQFAGPHL 420
Db  307  VTHAFMDIHDIYLEQFAGEGRTARFGNDFEPVAWSRDRIAVRGGADREFDIVETRHGPVI 366

Qy  421  AANPQTDRDGHVLSSQSTGSSNTEFSVDYLALICGFGAPLLARLLFYLERCDAGAFTG-- 478
Db  367  AGDP----RDGAALTLRSVQFAETDLSFDCLTRMP--GASTVAQLY------DATRGWGLI 415

Qy  479  GH-----GDALKYVTGTFDSEIPCSLCEKHTRPVCAHTTVHRLR----QRMRFGQATRQ 529
Db  416  DHNLVAGDVAGSIGHLVRARVPSRPRENGWLPVPGWNSGEHEWRGWIPHEAMPR---VIDP 472

Qy  530  PIGVFGTMNSQY----------SDCDPLGNYAPY------LILRKPGDQTEAAKATMQD 572
Db  473  PGGIIVTANNRVVADDHPDYLCTDCHP----PYRAERIMKRLVANPAFAVDDAAAIHAD 527

Qy  573  TYRATLERLFIDLEQERLLDRGA--PCSSEGLSSVIV----------DHPTFRRIL 616
```

```
Db  528  TLSP-----HVGLLRRRLEALGARDDSAAEGLRQMLVAWDGRMDAAASVASAYNAFRRAL 582
Qy  617  DTL--RARIEQTTTQ-----------------FMKVLVETRDYKIREG-----LSEA- 649
Db  583  TRLVTDRSGLEQAISHPFAAVAPGPGQVMWAVPTLLRDDDAGMLKGWSWDQALSEAL 642

Qy  650  -----------------------THSMALTFDPYSGAFCP 666
Db  643  SVASQNLTGRSWGEEHRPRFTHPLATQFPAWAGLLNP 679
```

RESULT 25
US-08-633-760-44
; Sequence 44, Application US/08633760
; Patent No. 580429
; GENERAL INFORMATION:
;   APPLICANT: NIWA, MINEO
;   APPLICANT: SAITO, YOSHIMASA
;   APPLICANT: FUJIMURA, TAKAO
;   APPLICANT: ISHII, YOSHINORI
;   APPLICANT: NOGUCHI, YUJI
;   TITLE OF INVENTION: A NEW CEPHALOSPORIN C ACYLASE
;   NUMBER OF SEQUENCES: 64
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
;   ADDRESSEE: P.C.
;   STREET: 1755 JEFFERSON DAVIS HIGHWAY, SUITE 400
;   CITY: ARLINGTON
;   STATE: VIRGINIA
;   COUNTRY: USA
;   ZIP: 22202
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/633,760
;   FILING DATE: 01-MAY-1996
;   CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
;   NAME: OBLON, NORMAN F.
;   REGISTRATION NUMBER: 24,618
;   REFERENCE/DOCKET NUMBER: 18-929-0 PCT
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (703) 413-3000
;   TELEFAX: (703) 413-2220
;   TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 44:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 774 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-633-760-44

```
Query Match               1.6%;    Score 103;   DB 1;   Length 774;
Best Local Similarity   20.6%;     Pred. No. 0.97;
Matches 145;  Conservative  77;  Mismatches 241;  Indels 242;  Gaps  37;

Qy  109  LTR--ACNAARERFGFSRCQGPPVDGAVETTGAE-ICTR----LGLEPENTILYLVVTAL 161
Db   70  LTRRKALGRAAEWLG--AEAAEADILVRRLGMEKVCRRDFEALGVEAKD--------M 117

Qy  162  FKEAVFMCNVFLHYGGLDIVHINHGDVIRIPLFPVQLFMPDVNRLVPDPFNTHH----R 216
Db  118  LRAYVAGVNAFLASGA-------------PL-PVEYGLLGAE---PEPWEPWHSIAVMR 159

Qy  217  SIGEGFVYPTPFYNTGLCHLIHDCVIAPMAVALRVRNVTAV-----ARGAAHLAFDENHEG 272
Db  160  RLG----------------LLAGSVWFKLWRMLALPVVGAANALKLRYDDGGRD 197
```

Qy   273 AV-LPPDITYTYFQSSSGTTARGARRNDVNSTSKFSPSGGFER------RLAS---IM 322
Db   198 LLCIPPGAEADRLEADLATLRPAVDALLKAMGDASDAAGGGSNNWAVAPGRTATGRPIL 257
Qy   323 AADTALHAEVIFNTGIYEETPTDIKEWPMFIGMEGTLPRLNALGSYTARVAGVIGAMVFS 382
Db   258 AGDPHRVFEI---PGMYAQHHLACDRFDM-IGL--TVP----------GVPGFPHFA 298
Qy   383 PNSA--------------LYLTEVEDSGMTE----------AKDGGPGPSFNRF 412
Db   299 HNGKVAYCVTHAFMDIHDLYLEQFAGEGRTARFGNDFEPVAWSRDRIAVRGGADREFDIV 358
Qy   413 YQFAGPHLAANPQTDRDGHVLSSQSTGSSNTEFSVDYLALICGFGAPLLARLLFYLERCD 472
Db   359 ETRHGPVIAGDP---RDGAALTLRSVQFAETDLSFDCLTRMP--GASTVAQLY------D 407
Qy   473 AGAFTG--GH----GDALKYVTGTPDSEIPCSLCEKHTRPVCAHTTVHRLR------QRMP 521
Db   408 ATRGWGLIDHNLVAGDVAGSIGHLVRARVPSRPRENGWLPVPGWSGEHWRGWIPHEAMP 467
Qy   522 RFGQATRQPIGVFGTMNSQY---------SDCDPLGNYAPY------LILRKPGDQTE 564
Db   468 R---VIDPPCGIIVTANNRVVADDHPDYLCTDCHP-----PYRAERIMKRLVANPAFAVD 519
Qy   565 AAKATMQDTYRATLERLFIDLEQERLLDRGA--PCSSEGLSSVIV------D 608
Db   520 DAAAIHADTLSP-----HVGLLRRRLEALGARDDSAAEGLRQMIVAWDGRMDAASEVASA 574
Qy   609 HPTFRRILDTL---RARIEQTTQ----------------FMKVLVETRDYKIREG--- 645
Db   575 YNAFRRALTRLIVTDRSGLEQAISHPFAAVAPGVSPQGQVWWAVPTLLRDDDAGMLKGWSW 634
Qy   646 ---LSEA-----------THSMALITFDPYSGAFCP 666
Db   635 DQALSEALSVASQNLTGRSWGEEHRPRFTHPLATQFPAWAGLLNP 679

RESULT 26
US-09-408-020-4
; Sequence 4, Application US/09408020
; Patent No. 6632937
; GENERAL INFORMATION:
; APPLICANT: Swanson, Ronald V.
; APPLICANT: Feldman, Robert A.
; APPLICANT: Schleper, Christa
; FILE REFERENCE: DCORP.002A
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
; CURRENT APPLICATION NUMBER: US/09/408,020
; CURRENT FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/102,294
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
;   LENGTH: 3472
;   TYPE: PRT
;   ORGANISM: Cenarchaeum symbiosum
US-09-408-020-4

Query Match   1.6%;   Score 103; DB 4; Length 3472;
Best Local Similarity   20.2%;   Pred. No. 16;
Matches   98;   Conservative   51;   Mismatches   175;   Indels   160;   Gaps   24;

Qy   82 LTTSHEYPSVFVFHGGKHVLPSSAAPNLTRACNAARERFGPSRCCQGPPVDGAVETTGAEI 141
Db   928 LAVSGYAEPSLVF--GRHAVPGAAGGTPFSQIGNATELVG--SIPNPTLDFGTTLTGA-- 981
Qy   142 CTRLGLEPENTILYLVVTALFKEAVFMCNVFLHY-----GGLDIVHINHGGVIRIPLFPV 196
Db   982 ---AFPSADGTVFFLSDGPTGRVFYPYSLNIFPDISSAAPGGFVIVPGVSDI-------- 1029
Qy   197 QLFMPD-VNRLVPDPFNTHHRSIGEG-FVYPTPFYNTGLCHLIHDCVIAPMAVALRVRNV 254

US-08-070-165F-6
; Sequence 6, Application US/08070165F
; Patent No. 5750365
; GENERAL INFORMATION:
; APPLICANT: Chiu, Ing-Ming
; APPLICANT: Poulin, Matthew L
; TITLE OF INVENTION: Acidic Fibroblast Growth Factor (aFGF)
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Ing-Ming Chiu
;   STREET: S2052 Davis Medical Research Center, 480 West
;   STREET: 9th Avenue
;   CITY: Columbus
;   STATE: Ohio
;   COUNTRY: USA
;   ZIP: 43210
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/070,165F
;   FILING DATE:
;   CLASSIFICATION: 435
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (614)-293-8093
;   TELEFAX: (614)-293-5631
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 729 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-070-165F-6

Query Match   1.6%;   Score 102; DB 1; Length 729;
Best Local Similarity   20.0%;   Pred. No. 1.1;
Matches 111;   Conservative   69;   Mismatches 206;   Indels 168;   Gaps   26;

Qy   355 MEGTLPRLNALGSYTARVAGVIGAMVFSPNSALYLTEVEDS----------GMTEAKDG 403
Db   128 MESVVP--SDEGNYTCIMENEYGSI----NHTYHLDVVERSPHRPILQAGLPANTTTKVG 181
Qy   404 GPGPSFNRFYQFAGPHL--------AANPQTDRDGH----VLSSQSTGSSNTEFSVDYLAL 452

Db 1030 -AFSADGRNMLVADETGGIHRYLARSPYEIGTDFIKSSLGEVETFSAAP-----RVQDL 1083
Qy   255 TAVARGAAHLAPDENHSGAVLPPDITYTYFQSSSGTTARGARRNDVNSTSKPSP---S 311
Db 1084 AGIA-----------FSHDGMIM-----------LAAGGSGS-----------VHRYSLPSPYAVS 1116
Qy   312 G-----------GFF-----RRLASIMAADTALHAEVIFNTGIYEETPTDIKEWPM 351
Db 1117 GAKYEETAMIGGSPSGLEFSSDGLRMFVPDAGSETAAVYGLAAPYGIGEAEFLP----PL 1172
Qy   352 FIGM----EGTL-----PRLNALGSYT--------ARVAGVIGAMVFSPNSALYLT 390
Db 1173 FLGVGAEEATLSPDGRHILVPGRPGLSQYSLFSTNLELCAEPRGIDGG---SCEDGIYAF 1229
Qy   391 EVEDSG---MTEAKDGGPGPSFNRFYQFAGPHLAA----------------------- 422
Db 1230 ESPGRGEGVSLAASITAADGPGIGELHGFAGPPMPAPVMEQVTLDSREGTLRVRLDRTVD 1289
Qy   423 ----NPQ---TDRDGHVLSSQSTGSSNTEFSVDYLALICGFGAPLLARLLFYLERCDAG 474
Db 1290 VDTVRPYKMWVEDSDG----SQTTLANSTLLNAENSNI----------LLFRLDDAAAG 1334
Qy   475 AFTG 478
Db 1335 KISG 1338

```
Query Match                1.6%;  Score 102;  DB 2;  Length 729;
Best Local Similarity     20.0%;  Pred. No. 1.1;
Matches 111;  Conservative 69;  Mismatches 206;  Indels 168;  Gaps 26;

Qy  355  MEGTLPRLNALGSYTARVAGVIGAMVFSPNSALVLTEVEDS----------GMTEAKDG 403
            :  |:.|:|::|:                 |::       |||
Db  128  MESVVP--SDEGNYTCIMENEYGSI---NHTYHLDVVERSPHRPILQAGLPANTTTKVG 181

Qy  404  GPGPSFNRFYQFAGPHL------AANPQTDRDGH----VLSSQSTGSSNTEFSVDYLAL 452
            |  .  . |:  |:||     :  |  |     ||   |
Db  182  GDAEFVCKVYSDAQPHIQWIRHFELNGSKIGPDGHPYLKVLKAAGVNTTDKEIEVLYVRN 241

Qy  453  ICGFGAPLLARLLFYLERCDAGAFT--GGHGDALKYVTGTF------DSEIPCS------ 498
            |||                    :    ||                   :
Db  242  VS----------FE--DAGEYTCLAGNSTGISYHTAWLTVLPDEERELDSSSEYTEI 286

Qy  499  ------------LCEKHTRPVC----------AHTTVHRLRQRMPRFGQAT-------- 527
                      |||                 :|
Db  287  AIYCVGGFLITCMIGTIMVCHMKGRGKKSDFSSPPAVHKLSKSLPLRRQVTVSADSSSSM 346

Qy  528  --RQPIGVFGTMNSQYSDCDPLGNYAPY-----------LILRKP-GD----------- 561
            | |:|  |:: |:    :|              |::||| ||
Db  347  NSNTPLVRITTRLSSNNDTHLLAGVSEYELPEDPKWEYPREKLTLGKPLGEGCFGQVVMA 406

Qy  562  ------------QTEAAKATMQDTYRATLERLFIDLEQERLLDR--------GAPCSSE 600
                      |::  :::               |:|     ||        : :::|
Db  407  EAVGIDKDRPKDAATVAVKMLKDDATEKDLSDLVSEMEMKMIGKHKNIINLLGA-CTQD 465

Qy  601  GLSSVIVDHPT---FRRILDTLRARIEQTTTQFMKVLVETRDYKIREGLSEATHSMALTF 657
            |::|  |        |||   |           |:|   |||        :||  |
Db  466  GPLYIVEYASKGNLREYLRTRRPPGMEYSFDINRIPEEQMTFK---DLVSCTYQLARGM 522

Qy  658  DPYSGAFC----------PITNFLVKRTHLAVVQDLALSQ--CHCVFYGQQVEGRNFRNQFQPVL 710
            : |:  ||          |::  :     :|                   |
Db  523  EYLASQKCIHRDLAARNVLVTETNVMKIADFGLARDINNIDYYKKTTNGR----------LPVK 576

Qy  711  RRRFVDLFNGGFISTRSITVTLSEGPVSAPNPTLGQDAPAGRTFDGDLARVSV-EVIRDI 769
            |||                              |          |          |::|:|
Db  577  WMAPEALFDRVYTHQSDV---WSFGVLMWEIFTLG----GSPYPG----IPVEELFKLL 624

Qy  770  RVKNRVVFSGNCTN 783
            : |:  ||||||
Db  625  KEGHRMDKPGNCTN 638
```

RESULT 29
US-07-747-901A-3
; Sequence 3, Application US/07747901A
; Patent No. 5192678
GENERAL INFORMATION:
  APPLICANT: Iwami, Morita
  APPLICANT: Aramori, Ichiro
  APPLICANT: Fukagawa, Masao
  APPLICANT: Isogai, Takao
  APPLICANT: Kojo, Hitoshi
  TITLE OF INVENTION: CEPHALOSPORIN C ACYLASE
  NUMBER OF SEQUENCES: 3
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
    ADDRESSEE: P.C.
    STREET: 1755 Jefferson Davis Highway, Fourth Floor
    CITY: Arlington
    STATE: Virginia
    ZIP: 22202
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.25
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/07/747,901A
    FILING DATE: 19910820
    CLASSIFICATION: 435

```
Db  182  GDAEFVCKVYSDAQPHIQWIRHFELNGSKIGPDGHPYLKVLKAAGVNTTDKEIEVLYVRN 241

Qy  453  ICGFGAPLLARLLFYLERCDAGAFT--GGHGDALKYVTGTF------DSEIPCS------ 498
Db  242  VS----------FE--DAGEYTCLAGNSTGISYHTAWLTVLPDEERELDSSSEYTEI 286

Qy  499  ------------LCEKHTRPVC----------AHTTVHRLRQRMPRFGQAT-------- 527
Db  287  AIYCVGGFLITCMIGTIMVCHMKGRGKKSDFSSPPAVHKLSKSLPLRRQVTVSADSSSSM 346

Qy  528  --RQPIGVFGTMNSQYSDCDPLGNYAPY-----------LILRKP-GD----------- 561
Db  347  NSNTPLVRITTRLSSNNDTHLLAGVSEYELPEDPKWEYPREKLTLGKPLGEGCFGQVVMA 406

Qy  562  ------------QTEAAKATMQDTYRATLERLFIDLEQERLLDR--------GAPCSSE 600
Db  407  EAVGIDKDRPKDAATVAVKMLKDDATEKDLSDLVSEMEMKMIGKHKNIINLLGA-CTQD 465

Qy  601  GLSSVIVDHPT---FRRILDTLRARIEQTTTQFMKVLVETRDYKIREGLSEATHSMALTF 657
Db  466  GPLYIVEYASKGNLREYLRTRRPPGMEYSFDINRIPEEQMTFK---DLVSCTYQLARGM 522

Qy  658  DPYSGAFC----------PITNFLVKRTHLAVVQDLALSQ--CHCVFYGQQVEGRNFRNQFQPVL 710
Db  523  EYLASQKCIHRDLAARNVLVTETNVMKIADFGLARDINNIDYYKKTTNGR----------LPVK 576

Qy  711  RRRFVDLFNGGFISTRSITVTLSEGPVSAPNPTLGQDAPAGRTFDGDLARVSV-EVIRDI 769
Db  577  WMAPEALFDRVYTHQSDV---WSFGVLMWEIFTLG----GSPYPG----IPVEELFKLL 624

Qy  770  RVKNRVVFSGNCTN 783
Db  625  KEGHRMDKPGNCTN 638
```

RESULT 28
US-08-885-418-6
; Sequence 6, Application US/08885418
; Patent No. 5925528
GENERAL INFORMATION:
  APPLICANT: Chiu, Ing-Ming
  APPLICANT: Poulin, Matthew L
  TITLE OF INVENTION: Acidic Fibroblast Growth Factor (aFGF)
  NUMBER OF SEQUENCES: 12
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Ing-Ming Chiu
    STREET: S2052 Davis Medical Research Center, 480 West
    STREET: 9th Avenue
    CITY: Columbus
    STATE: Ohio
    COUNTRY: USA
    ZIP: 43210
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.25
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/885,418
    FILING DATE:
    CLASSIFICATION: 435
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (614)293-8093
    TELEFAX: (614)293-5631
INFORMATION FOR SEQ ID NO: 6:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 729 amino acids
    TYPE: amino acid
    TOPOLOGY: linear
  MOLECULE TYPE: protein
US-08-885-418-6

GENERAL INFORMATION:
  APPLICANT: Iwami, Morita
  APPLICANT: Aramori, Ichiro
  APPLICANT: Fukagawa, Masao
  APPLICANT: Isogai, Takao
  APPLICANT: Kojo, Hitoshi
  TITLE OF INVENTION: CEPHALOSPORIN C ACYLASE
  NUMBER OF SEQUENCES: 3
  CORRESPONDENCE ADDRESS:
  ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
  ADDRESSEE: P.C.
  STREET: 1755 Jefferson Davis Highway, Fourth Floor
  CITY: Arlington
  STATE: Virginia
  ZIP: 22202
  COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: PatentIn Release #1.0, Version #1.25
  CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/07/935,312
  FILING DATE: 19920826
  CLASSIFICATION: 435
  ATTORNEY/AGENT INFORMATION:
  NAME: Oblon, No. 5320948man F.
  REGISTRATION NUMBER: 24,618
  REFERENCE/DOCKET NUMBER: 18-769-0 DIV
  TELECOMMUNICATION INFORMATION:
  TELEPHONE: (703)521-4500
  TELEFAX: (703)486-2347
  TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 3:
  SEQUENCE CHARACTERISTICS:
  LENGTH: 774 amino acids
  TYPE: AMINO ACID
  TOPOLOGY: linear
  MOLECULE TYPE: protein
US-07-935-312-3

Query Match   1.6%;   Score 102; DB 1; Length 774;
Best Local Similarity 20.6%; Pred. No. 1.2;
Matches 145; Conservative 77; Mismatches 241; Indels 242; Gaps 37;

Qy 109 LTR--ACNAARERFGFSRCQGPPVDGAVETTGAE-ICTR----LGLEPENTILYLVVTAL 161
Db   70 LTRRKALGRAAEWLG---AEAABADILVRRLGMEKVCRRDFBALGVEAKD------M 117

Qy 162 FKEAVFMCNVFLHYGGLDIVHINHGDVIRIPLFPVQLFMPDVNRLVPDPFNTHH-----R 216
Db 118 LRAYVAGVNAFLASGA---------PL-PVEYGLLGAE---PEPWEPWHSIAVMR 159

Qy 217 SIGEGFVYPTPFYNTGLCHLIHDCVIAPMAVALRVRNVTAV----ARGAAHLAFDENHEG 272
Db 160 RLG----------------LLMGSVWFKLWRMLALPVVGAANALKLRYDDGGRD 197

Qy 273 AV-LPPDITYTYFQSSSGTTARGARRNDVNSTSKPSPSGGFER------RLAS---IM 322
Db 198 LLCIPPGAEADRLEADLATLRPAVDALLKAMGGDASDAAGGGSNWAVAPGRTATGRPIL 257

Qy 323 AADTALHAEVIFNTGIYEETPTDIKEWPMFIGMEGTLPRLNALGSYTARVAGVIGAMVFS 382
Db 258 AGDPHRVFEI---PGMYAQHHLACDRFDM-IGL--TVP-----------GVPGFPHFA 298

Qy 383 PNSA----------LYLTEVEDSGMTE---------------------AKDGGPGSFNRF 412
Db 299 HNGKVAYCVTHAFMDIHDLYLEQPAGEGRTARFGNDFEPVAWSRDRIAVRGGADREFDIV 358

Qy 413 YQFAGPHLAANPQTDRDGHVLSSQSTGSSNTEFSVDYLALICGFGAPLIARLLFYLERCD 472
Db 359 ETRHGPVIAGDP---RDGAALTLRSVQFAETDLSFDCLITRMP--GASTVAQLY-----D 407

Qy 473 AGAFTG--GH-----GDALKYVTGTFDSEIPCSLCEKHTRPVCAHTTVHRLR-----QRMP 521

ATTORNEY/AGENT INFORMATION:
  NAME: Oblon, No. 5192678man F.
  REGISTRATION NUMBER: 24,618
  REFERENCE/DOCKET NUMBER: 18-709-0
  TELECOMMUNICATION INFORMATION:
  TELEPHONE: (703)521-4500
  TELEFAX: (703)486-2347
  TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 3:
  SEQUENCE CHARACTERISTICS:
  LENGTH: 774 amino acids
  TYPE: AMINO ACID
  TOPOLOGY: linear
  MOLECULE TYPE: protein
US-07-747-901A-3

Query Match   1.6%;   Score 102; DB 1; Length 774;
Best Local Similarity 20.6%; Pred. No. 1.2;
Matches 145; Conservative 77; Mismatches 241; Indels 242; Gaps 37;

Qy 109 LTR--ACNAARERFGFSRCQGPPVDGAVETTGAE-ICTR----LGLEPENTILYLVVTAL 161
Db   70 LTRRKALGRAAEWLG---AEAABADILVRRLGMEKVCRRDFBALGVEAKD------M 117

Qy 162 FKEAVFMCNVFLHYGGLDIVHINHGDVIRIPLFPVQLFMPDVNRLVPDPFNTHH-----R 216
Db 118 LRAYVAGVNAFLASGA---------PL-PVEYGLLGAE---PEPWEPWHSIAVMR 159

Qy 217 SIGEGFVYPTPFYNTGLCHLIHDCVIAPMAVALRVRNVTAV----ARGAAHLAFDENHEG 272
Db 160 RLG----------------LLMGSVWFKLWRMLALPVVGAANALKLRYDDGGRD 197

Qy 273 AV-LPPDITYTYFQSSSGTTARGARRNDVNSTSKPSPSGGFER------RLAS---IM 322
Db 198 LLCIPPGAEADRLEADLATLRPAVDALLKAMGGDASDAAGGGSNWAVAPGRTATGRPIL 257

Qy 323 AADTALHAEVIFNTGIYEETPTDIKEWPMFIGMEGTLPRLNALGSYTARVAGVIGAMVFS 382
Db 258 AGDPHRVFEI---PGMYAQHHLACDRFDM-IGL--TVP-----------GVPGFPHFA 298

Qy 383 PNSA----------LYLTEVEDSGMTE---------------------AKDGGPGSFNRF 412
Db 299 HNGKVAYCVTHAFMDIHDLYLEQPAGEGRTARFGNDFEPVAWSRDRIAVRGGADREFDIV 358

Qy 413 YQFAGPHLAANPQTDRDGHVLSSQSTGSSNTEFSVDYLALICGFGAPLIARLLFYLERCD 472
Db 359 ETRHGPVIAGDP---RDGAALTLRSVQFAETDLSFDCLITRMP--GASTVAQLY-----D 407

Qy 473 AGAFTG--GH----GDALKYVTGTFDSEIPCSLCEKHTRPVCAHTTVHRLR-----QRMP 521
Db 408 ATRGWGLIDHNLVAGDVAGSIGHLVRARVPSRPRENGWLPVPGWSGEHEWRGWIPHEAMP 467

Qy 522 RFGQATRQPIGVFGTMNSQY---------SDCDPLGNYAPY---------LILRKPGDQTE 564
Db 468 R---VIDPPGGIIVTANRRVVADDHPDYLCTDCHP-----PYRAERIMKRLVANPAFAVD 519

Qy 565 AAKATMQDTYRATLERLFIDLEQERLLDRGA--PCSSEGLSSVIV----------D 608
Db 520 DAAAIHADTLSP-----HVGLLRRRLEALGARDDSAAEGLRQMLVAWDGRMDAASEVASA 574

Qy 609 HPTFRRILDTL---RARIEQTTQ------------------FMKVLVETRDYKIREG---645
Db 575 YNAFRRALTRLVTDRSGLEQAiSHPPAAVAPGVSPGGQVWWAVPTLLRDDDDAGMLKGWSW 634

Qy 646 --LSEA-----------------------THSMALTFDPYSGAFCP 666
Db 635 DQALSEALSVASQNLTGRSWGEHRPRFTHPLATQFPAWAGLLNP 679

RESULT 30
US-07-935-312-3
; Sequence 3, Application US/07935312
; Patent No. 5320948

```
Qy  162 FKEAVFMCNVFLHVGGLDIVHINHGDVIRIPLFPVQLFMPDVNRLVPDPFNTHH-----R 216
            ||                    : |  |  |        :||:
Db  118 LRAYVAGVNAFLASGA-------------------PL-PVEYGLLGAE--PEPWEPWHSIAVMR 159

Qy  217 SIGEGFVYPTPFYNTGLCHLIHDCVIAPM--AVALRVRNVTAVARGAAHLAPDENHEGAV 274
             |                |  :|:|  |:||:
Db  160 RLG------------------LLLGSVWFKLWRALALPV----VGAANALKLRYDDGGRDLL 199

Qy  275 -LPPDITYTYFQSSSSGTTTARGARRNDVNSTSKPSPSGGFER-------RLAS---IMAA 324
          :||          |||                           : ||:
Db  200 CIPPGAEADRLEADLIATLRPAVDALLKAMGGDASDAAGGGSNNWAVAPGRTATGRPILAG 259

Qy  325 DTALHAEVIFNTGIYEETPTDIKEWPMFIGMEGTLPRLNALGSYTARVAGVIGAMVFSPN 384
          |:       :           |::
Db  260 DPHRVFEI---PGYYAQHHLACDRFDM-IGL--TVP------------GVPGFPHFAHN 300

Qy  385 SA--------------------LYITEVEDSGMTE----------------AKDGGPGPSFNRFYQ 414
          ||                   :|||
Db  301 GKVAYCVTHAFMDIHDLYLEQFAGEGRTARFGNDEPVAWSRDRIAVRGGADREFDIVET 360

Qy  415 FAGPHLAANPQTDRDGHVLSSQSTGSSNTEFSVDYLALICGFGAPLLARLLFYLERCDAG 474
          |:          :||            |:|   |           ::
Db  361 RHGPVIAGDP---RDGAAILTRSVQFAETDLSFDCLTRMP------GASTVAQLY------DAT 409

Qy  475 AFTG--GH----GDALKYVTGTFDSBIPCSLCEKHTRPVCAHTTVHRLR----QRMPRF 523
             |  ||       ||  |        :||
Db  410 RGWGLIDHNLVAGDVAGSIGHLVRARVPSRPRENGWLPVPGWSGEHEWRGWIPHEAMPR- 468

Qy  524 GQATRQPIGVFGTMNSQY-----------SDCDPLGNYAPY------LILRKPGDQTEAA 566
           ||  | |              ||||            :||||
Db  469 --VIDPPGGIIVTANNRVVADDHPDYLCTDCHP-----PYRAERIMKRLVANFAFAVDDA 521

Qy  567 KATMQDTYRATLERLFIDLEQERLLDRGA-PCSSEGLSSVIV----------DHP 610
           |||||||||||||||||||||||||||  |||||||||||
Db  522 AAIHADTLSP-----HVGLLRRRLEALGARDDSAAEGLRQMLVAWDGRMDAASEVASAYN 576

Qy  611 TFRRILDTL--RARIEQTTQ-----------FMKVLVETRDYKIREG------ 645
           ||||| ||  ||||||||             ||||||||||||||
Db  577 AFRRALTRLVTDRSGLEQAISHPFAAVAPGVSPQGQVWWAVPTLLRDDDAGMLKGWSWDQ 636

Qy  646 -LSEA----------------------THSMALTFDPYSGAFCP 666
           |||                        ||||||||||||||
Db  637 ALSEALSVASQNLTGRSWGEEHRPRFTHPLATQFPAWAGLLNP 679
```

RESULT 32
US-08-019-870-1
; Sequence 1, Application US/08019970
; Patent No. 5336613
; GENERAL INFORMATION:
;   APPLICANT: NIWA, MINEO
;   APPLICANT: YOSHIMASA, SAITO
;   APPLICANT: SASAKI, HITOSHI
;   APPLICANT: ISHII, YOSHINORI
;   TITLE OF INVENTION: A NEW CEPHALOSPORIN C ACYLASE
;   NUMBER OF SEQUENCES: 42
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
;   ADDRESSEE: P.C.
;   STREET: 1755 S. Jefferson Davis Highway, Suite 400
;   CITY: Arlington
;   STATE: Virginia
;   COUNTRY: U.S.A.
;   ZIP: 22202
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/019,870
;   FILING DATE: 19930219
;   CLASSIFICATION: 435

```
Db  408 ATRGWGLIDHNLVAGDVAGSIGHLVRARVPSRPRENGWLPVPGWSGEHEWRGWIPHEAMP 467
             |  |  ||       ||  |        :||
Qy  522 RFGQATRQPIGVFGTMNSQY-------SDCDPLGNYAPY------LILRKPGDQTE 564
Db  468 R---VIDPPGGIIVTANNRVVADDHPDYLCTDCHP-----PYRAERIMKRLVANPAFAVD 519
Qy  565 AAKATMQDTYRATLERLFIDLEQERLLDRGA--PCSSEGLSSVIV---------D 608
             |||||||||||||||||||||||||||  |||||||||||
Db  520 DAAAIHADTLSP------HVGLLRRRLEALGARDDSAAEGLRQMLVAWDGRMDAASEVASA 574
Qy  609 HPTFRRILDTL---RARIEQTTQ--------------FMKVLVETRDYKIREG--- 645
            ||||| ||   ||||||||               ||||||||||||||
Db  575 YNAFRRALTRLVTDRSGLEQAISHPFAAVAPGVSPQGQVWWAVPTLLRDDDDAGMLKGWSW 634
Qy  646 ---LSEA----------------------THSMALTFDPYSGAFCP 666
              |||                        ||||||||||||||
Db  635 DQALSEALSVASQNLTGRSWGEEHRPRFTHPLATQFPAWAGLLNP 679
```

RESULT 31
US-08-633-760-50
; Sequence 50, Application US/08633760
; Patent No. 5804429
; GENERAL INFORMATION:
;   APPLICANT: NIWA, MINEO
;   APPLICANT: SAITO, YOSHIMASA
;   APPLICANT: FUJIMURA, TAKAO
;   APPLICANT: ISHII, YOSHINORI
;   APPLICANT: NOGUCHI, YUJI
;   TITLE OF INVENTION: A NEW CEPHALOSPORIN C ACYLASE
;   NUMBER OF SEQUENCES: 64
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
;   ADDRESSEE: P.C.
;   STREET: 1755 JEFFERSON DAVIS HIGHWAY, SUITE 400
;   CITY: ARLINGTON
;   STATE: VIRGINIA
;   COUNTRY: USA
;   ZIP: 22202
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/633,760
;   FILING DATE: 01-MAY-1996
;   CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;   NAME: OBLON, NORMAN F.
;   REGISTRATION NUMBER: 24,618
;   REFERENCE/DOCKET NUMBER: 18-929-0 PCT
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (703) 413-3000
;   TELEFAX: (703) 413-2220
;   TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 50:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 774 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-633-760-50

Query Match   1.6%; Score 102; DB 1; Length 774;
Best Local Similarity 21.2%; Pred. No. 1.2;
Matches 149; Conservative 73; Mismatches 243; Indels 238; Gaps 38;

Qy 109 LTR--ACNAARERFGFSRCCGPPVDGAVETTGAE-ICTR----LGLEPENTILYLVVTAL 161
          ||| || ::|: |||:
Db   70 LTRRKALGRAAEWLG--ABAAEADILVRRLGMEKVCRRDFEALGVEAKD--------M 117

ATTORNEY/AGENT INFORMATION:
    NAME: Oblon, No. 5336613man F.
    REGISTRATION NUMBER: 24,618
    REFERENCE/DOCKET NUMBER: 18-791-0
TELECOMMUNICATION INFORMATION:
    TELEPHONE: (703) 413-3000
    TELEFAX: (703) 413-2220
    TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
    LENGTH: 773 amino acids
    TYPE: amino acid
    TOPOLOGY: linear
    MOLECULE TYPE: protein
US-08-019-870-1

Query Match   1.6%;   Score 101.5; DB 1; Length 773;
Best Local Similarity   21.9%;   Pred. No. 1.4;
Matches   91; Conservative 41; Mismatches 139; Indels 145; Gaps 19;

Qy   372 VAGVIGAMVFSPNSA-----------------LYLTEVEDSGMTE--------------AK 401
            ||||| |||||||| :
Db   287 VPGVPGFPHFAHNGKVAYXVTHAFMDIHDLYLEQFAGEGRTARFGNDFEPVAWSRDRIAV 346

Qy   402 DGGPGPSFNRFYQPAGPHLAANPQTDRDGHVLSSQSTGSSNTEFSVDYLALICGFGAPLL 461
            || | | || || : :|| |||
Db   347 RDGAALTLRSVQFAETDLSFDCLTRMP--GASTV 401

Qy   462 ARLLFYLERCDAGAFTG--GH-----GDALKYVTGTFDSEIPCSLCEKHTRPVCAHTTVHR 515
            :| :: : :: ||
Db   402 AQLY------DATRGWGLIDHNLVAGDVAGSIGHLVRARVPSRPRENGWLPVPGWSGEHE 455

Qy   516 LR------QRMPRFGQATRQPIGVFGTMNSQY-----------SDCDPLGNYAPY----- 553
            :| |: ||
Db   456 WRGWIPHEAMPR---VIDPPGGIIVTANNRVVADDHPDYLCTDCHP----PYRAERIMK 507

Qy   554 LILRKPGDQTEAAKATMQDTYRATLERLFIDLEQERLLDRGA-PCSSEGLSSVIV----- 607
            || :| ::| | || || : ::
Db   508 RLVANPAFAVDDAAAIHADTLSP-----HVGLLRRRLEALGARDDSAAEGLRQMLVAWDG 562

Qy   608 --------DHPTFRRILDTL---RARIEQTTQ----------------FMKVLVET 637
                    |||||| | : :: || :
Db   563 RMDAASEVASAYNAFRRALTRLVTDRSGLEQAISHPFAAVAPGVSPQGQVWWAVPTLLRD 622

Qy   638 RDYKIREG-------LSEA----------------THSMALTFDPYSGAFCP 666
            :: :   ::
Db   623 DDAGMLKGWSWDQALSEALSVASQNLTGRSWGEEHRPRFTHPLATQFPAWAGLLNP 678

RESULT 33
US-08-019-870-6
; Sequence 6, Application US/08019870
; Patent No. 5336613
; GENERAL INFORMATION:
    APPLICANT: NIWA, MINEO
    APPLICANT: YOSHIMASA, SAITO
    APPLICANT: SASAKI, HITOSHI
    APPLICANT: ISHII, YOSHINORI
    TITLE OF INVENTION: A NEW CEPHALOSPORIN C ACYLASE
    NUMBER OF SEQUENCES: 42
    CORRESPONDENCE ADDRESS:
        ADDRESSE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
        STREET: 1755 S. Jefferson Davis Highway, Suite 400
        CITY: Arlington
        STATE: Virginia
        COUNTRY: U.S.A.
        ZIP: 22202
    COMPUTER READABLE FORM:
        MEDIUM TYPE: Floppy disk
        COMPUTER: IBM PC compatible
        OPERATING SYSTEM: PC-DOS/MS-DOS
        SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/019,870
    FILING DATE: 19930219
    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
    NAME: Oblon, No. 5336613man F.
    REGISTRATION NUMBER: 24,618
    REFERENCE/DOCKET NUMBER: 18-791-0
TELECOMMUNICATION INFORMATION:
    TELEPHONE: (703) 413-3000
    TELEFAX: (703) 413-2220
    TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
    LENGTH: 773 amino acids
    TYPE: amino acid
    TOPOLOGY: linear
    MOLECULE TYPE: protein
US-08-019-870-6

Query Match   1.6%;   Score 101.5; DB 1; Length 773;
Best Local Similarity   21.9%;   Pred. No. 1.4;
Matches   91; Conservative 41; Mismatches 139; Indels 145; Gaps 19;

Qy   372 VAGVIGAMVFSPNSA-----------------LYLTEVEDSGMTE--------------AK 401
            ||||| |||||||| :
Db   287 VPGVPGFPHFAHNGKVAYXVTHAFMDIHDLYLEQFAGEGRTARFGNDFEPVAWSRDRIAV 346

Qy   402 DGGPGPSFNRFYQPAGPHLAANPQTDRDGHVLSSQSTGSSNTEFSVDYLALICGFGAPLL 461
            || | | || || : :|| |||
Db   347 RGGADREFDIVETRHGPVIAGDP--RDGAALTLRSVQFAETDLSFDCLTRMP--GASTV 401

Qy   462 ARLLFYLERCDAGAFTG--GH-----GDALKYVTGTFDSEIPCSLCEKHTRPVCAHTTVHR 515
            :| :: : :: ||
Db   402 AQLY------DATRGWGLIDHNLVAGDVAGSIGHLVRARVPSRPRENGWLPVPGWSGEHE 455

Qy   516 LR------QRMPRFGQATRQPIGVFGTMNSQY-----------SDCDPLGNYAPY----- 553
            :| |: ||
Db   456 WRGWIPHEAMPR---VIDPPGGIIVTANNRVVADDHPDYLCTDCHP----PYRAERIMK 507

Qy   554 LILRKPGDQTEAAKATMQDTYRATLERLFIDLEQERLLDRGA-PCSSEGLSSVIV----- 607
            || :| ::| | || || : ::
Db   508 RLVANPAFAVDDAAAIHADTLSP-----HVGLLRRRLEALGARDDSAAEGLRQMLVAWDG 562

Qy   608 --------DHPTFRRILDTL---RARIEQTTQ----------------FMKVLVET 637
                    |||||| | : :: || :
Db   563 RMDAASEVASAYNAFRRALTRLVTDRSGLEQAISHPFAAVAPGVSPQGQVWWAVPTLLRD 622

Qy   638 RDYKIREG-------LSEA----------------THSMALTFDPYSGAFCP 666
            :: :   ::
Db   623 DDAGMLKGWSWDQALSEALSVASQNLTGRSWGEEHRPRFTHPLATQFPAWAGLLNP 678

RESULT 34
US-08-019-870-8
; Sequence 8, Application US/08019870
; Patent No. 5336613
; GENERAL INFORMATION:
    APPLICANT: NIWA, MINEO
    APPLICANT: YOSHIMASA, SAITO
    APPLICANT: SASAKI, HITOSHI
    APPLICANT: ISHII, YOSHINORI
    TITLE OF INVENTION: A NEW CEPHALOSPORIN C ACYLASE
    NUMBER OF SEQUENCES: 42
    CORRESPONDENCE ADDRESS:
        ADDRESSE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
        ADDRESSE: P.C.
        STREET: 1755 S. Jefferson Davis Highway, Suite 400
        CITY: Arlington
        STATE: Virginia
        COUNTRY: U.S.A.
        ZIP: 22202
    COMPUTER READABLE FORM:

```
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/019,870
FILING DATE: 19930219
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 533661man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-791-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 774 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-019-870-8
```

```
Query Match          1.6%;  Score 101.5;  DB 1;  Length 774;
Best Local Similarity 21.9%; Pred. No. 1.4;
Matches   91; Conservative 41; Mismatches 139; Indels 145; Gaps 19;

Qy  372 VAGVIGAMVFSPNSA----------LYLTEVEDSGMTE----------AK 401
        ||| :|     ||              |||
Db  288 VPGVPGFPHFAHNGKVAYSVTHAFMDIHDLYLEQFAGEGRTARFGNDFEPVAWSRDRIAV 347

Qy  402 DGGPGPSFNRFYQFAGPHLAANPQTDRDGHVLSSQSTGSSNTEFSVDYLALICGFGAPLL 461
        |::|        ||       |:  ||         :        :| |
Db  348 RGGADREFDIVETRHGPVIAGDP---RDGAALTLRSVQFAETDLSFDCLTRMP--GASTV 402

Qy  462 ARLLFYLERCDAGAFTG--GH----GDALKYVTGTFDSEIPCSLCEKHTRPVCAHTTVHR 515
        | ||         :          ::  |      :|      : |
Db  403 AQLY------DATRGWGLIDHNLVAGDVAGSIGHLVRARVPSRPRENGWLPVPGWSGEHE 456

Qy  516 LR-----QRMPRFGQATRQPIGVFGTMNSQY----------SDCDPLGNYAPY------- 553
        |:    :|            ||            :          ||
Db  457 WRGWIPHEAMPR---VIDPPGGIIVTANNRVVADDHPDYLCTDCHP------PYRAERIMK 508

Qy  554 LILRKPGDQTEAAKATMQDYRATLERLFIDLEQERLLDRGA-PCSSEGLSSVIV---- 607
        :|              |  ||          ::|            ||
Db  509 RLVANPAFAVDDAAAIHADTLSP-----HVGLLRRRLEALGARDDSAAEGLRQMLVAWDG 563

Qy  608 --------DHPTFRRILDTL---RARIEQTTQ----------------FMKVLVET 637
                 |||       ||     :|||             :
Db  564 RMDAASEVASAYNAFRRALTRLVTDRSGLEQAISHPFAAVAPGVSPQGQVWWAVPTLLRD 623

Qy  638 RDYKIREG------LSEA----------------THSMALTFDPYSGAFCP 666
        : :|        ||                     ::|
Db  624 DDAGMLKGWSWDQALSEALSVASQNLTGRSWGEEHRPRFTHPLATQFPAWAGLLNP 679
```

```
RESULT 35
US-08-019-870-11
; Sequence 11, Application US/08019870
; Patent No. 5336613
GENERAL INFORMATION:
APPLICANT: NIWA, MINEO
APPLICANT: YOSHIMASA, SAITO
APPLICANT: SASAKI, HITOSHI
APPLICANT: ISHII, YOSHINORI
TITLE OF INVENTION:  A NEW CEPHALOSPORIN C ACYLASE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
```

```
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/019,870
FILING DATE: 19930219
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 533661man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-791-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 774 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-019-870-11
```

```
Query Match          1.6%;  Score 101.5;  DB 1;  Length 774;
Best Local Similarity 21.9%; Pred. No. 1.4;
Matches   91; Conservative 41; Mismatches 139; Indels 145; Gaps 19;

Qy  372 VAGVIGAMVFSPNSA----------LYLTEVEDSGMTE----------AK 401
        ||| :|     ||              |||
Db  288 VPGVPGFPHFAHNGKVAYCVTHAFMDIHDLYLEQFAGEGRTARFGNDFEPVAWSRDRIAV 347

Qy  402 DGGPGPSFNRFYQFAGPHLAANPQTDRDGHVLSSQSTGSSNTEFSVDYLALICGFGAPLL 461
        |::|        ||       |:  ||         :        :| |
Db  348 RGGADREFDIVETRHGPVIAGDP---RDGAALTLRSVQFAETDLSFDCLTRMP--GASTV 402

Qy  462 ARLLFYLERCDAGAFTG--GH----GDALKYVTGTFDSEIPCSLCEKHTRPVCAHTTVHR 515
        | ||         :          ::  |      :|      : |
Db  403 AQLY------DATRGWGLIDHNLVAGDVAGSIGHLVRARVPSRPRENGWLPVPGWSGEHE 456

Qy  516 LR-----QRMPRFGQATRQPIGVFGTMNSQY----------SDCDPLGNYAPY------- 553
        |:    :|            ||            :          ||
Db  457 WRGWIPHEAMPR---VIDPPGGIIVTANNRVVADDHPDYLCTDCHP------PYRAERIMK 508

Qy  554 LILRKPGDQTEAAKATMQDYRATLERLFIDLEQERLLDRGA-PCSSEGLSSVIV---- 607
        :|              |  ||          ::|            ||
Db  509 RLVANPAFAVDDAAAIHADTLSP-----HVGLLRRRLEALGARDDSAAEGLRQMLVAWDG 563

Qy  608 --------DHPTFRRILDTL---RARIEQTTQ----------------FMKVLVET 637
                 |||       ||     :|||             :
Db  564 RMDAASEVASAYNAFRRALTRLVTDRSGLEQAISHPFAAVAPGVSPQGQVWWAVPTLLRD 623

Qy  638 RDYKIREG------LSEA----------------THSMALTFDPYSGAFCP 666
        : :|        ||                     ::|
Db  624 DDAGMLKGWSWDQALSEALSVASQNLTGRSWGEEHRPRFTHPLATQFPAWAGLLNP 679
```

Search completed: June 3, 2004, 07:15:17
Job time : 34 secs

```
                GenCore version 5.1.6
        Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:    June  3, 2004, 07:04:28 ; Search time 553 seconds
                                     (without alignments)
                        612.026 Million cell updates/sec

Title:            US-09-769-699-2
Perfect score:    6294
Sequence:         1 MENTQKTVTVPTGPLGVYA.........DELPDLSGIPIKHGNITMEM 1203

Scoring table:    BLOSUM62
                  Gapop 10.0 , Gapext 0.5

Searched:         1155919 seqs, 281338677 residues

Total number of hits satisfying chosen parameters:    1155919

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 100 summaries

Database :   Published Applications AA:*
         1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
         2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
         3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
         4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
         5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
         6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
         7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
         8: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
         9: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
        10: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
        11: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
        12: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
        13: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
        14: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
        15: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
        16: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
        17: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
        18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Query Length	DB	ID	Description
1	6294	100.0	1203	12	US-09-769-699-2	Sequence 2, Appli
2	3054	48.5	1452	13	US-10-050-673-2	Sequence 200, Appli
3	3015.5	47.9	1196	14	US-10-200-562-200	Sequence 200, App
4	3015.5	47.9	1196	14	US-10-237-551-232	Sequence 232, App
5	3015.5	47.9	1196	14	US-10-237-551-231	Sequence 231, App
6	788	12.5	274	14	US-10-237-551-230	Sequence 230, App
7	736	11.7	248	14	US-10-237-551-230	Sequence 9121, Ap
8	123.5	2.0	2597	12	US-10-156-761-9121	Sequence 34, Appl
9	123.5	2.0	2597	12	US-10-454-351-34	Sequence 358, App
10	123	2.0	1074	12	US-10-206-576-358	Sequence 394, App
11	123	2.0	1074	12	US-10-206-576-394	Sequence 45763, A
12	121	1.9	2358	12	US-10-282-122A-45763	Sequence 2, Appli
13	120.5	1.9	2597	9	US-09-905-129-2	Sequence 10, Appl
14	120.5	1.9	2597	9	US-09-905-129-10	Sequence 13, Appl
15	120.5	1.9	2597	9	US-09-905-129-13	Sequence 13, Appl
16	120.5	1.9	2597	9	US-09-991-630-2	Sequence 2, Appli
17	120.5	1.9	2597	9	US-09-991-630-10	Sequence 10, Appl
18	120.5	1.9	2597	9	US-09-991-630-13	Sequence 13, Appl
19	120.5	1.9	2597	12	US-10-454-351-2	Sequence 2, Appli
20	120.5	1.9	2597	12	US-10-454-351-10	Sequence 10, Appl
21	120.5	1.9	2597	12	US-10-454-351-13	Sequence 13, Appl
22	120.5	1.9	2597	12	US-09-729-485A-2	Sequence 2, Appli
23	120.5	1.9	2597	12	US-09-729-485A-10	Sequence 10, Appl
24	120.5	1.9	2597	12	US-09-729-485A-13	Sequence 13, Appl
25	120.5	1.9	2597	12	US-09-802-318-2	Sequence 2, Appli
26	120.5	1.9	2597	12	US-09-802-318-10	Sequence 10, Appl
27	120.5	1.9	2597	12	US-09-802-318-13	Sequence 13, Appl
28	120	1.9	5245	14	US-10-329-079-11	Sequence 11, Appl
29	118	1.9	452	12	US-10-425-114-71520	Sequence 71520, A
30	118	1.9	19608	15	US-10-084-846A-8	Sequence 8, Appli
31	114.5	1.8	1479	12	US-10-231-956A-325	Sequence 325, App
32	114.5	1.8	1496	12	US-10-211-462-87	Sequence 87, Appl
33	114.5	1.8	1496	14	US-10-021-660-125	Sequence 125, App
34	114.5	1.8	1496	15	US-10-331-498A-28	Sequence 28, Appl
35	114.5	1.8	1498	12	US-10-276-774-1957	Sequence 1957, Ap
36	114.5	1.8	1498	12	US-10-243-552-899	Sequence 899, App
37	113.5	1.8	1477	14	US-10-274-583-20	Sequence 20, Appl
38	113	1.8	1682	12	US-10-282-122A-64702	Sequence 64702, A
39	113	1.8	1787	12	US-10-282-122A-62625	Sequence 62625, A
40	113	1.8	2505	12	US-10-205-331-20	Sequence 20, Appl
41	112	1.8	943	12	US-10-282-122A-68197	Sequence 68197, A
42	112	1.8	3868	16	US-10-461-194-103	Sequence 103, App
43	112	1.8	6620	15	US-10-080-334-290	Sequence 290, App
44	112	1.8	6620	16	US-10-408-765A-2291	Sequence 2291, Ap
45	111.5	1.8	4317	12	US-10-282-122A-67862	Sequence 67862, A
46	111	1.8	5215	9	US-09-861-289-2	Sequence 2, Appli
47	111	1.8	5215	9	US-09-860-846-2	Sequence 2, Appli
48	111	1.8	5215	10	US-09-988-384B-2	Sequence 2, Appli
49	111	1.8	5215	10	US-09-836-821-2	Sequence 2, Appli
50	111	1.8	5215	14	US-10-271-889-45	Sequence 45, Appl
51	110.5	1.8	3069	9	US-09-712-363-246	Sequence 246, App
52	110	1.7	771	16	US-10-389-566-934	Sequence 934, App
53	110	1.7	784	12	US-10-282-122A-68623	Sequence 68623, A
54	110	1.7	1039	12	US-10-282-122A-77942	Sequence 77942, A
55	109.5	1.7	2630	13	US-10-077-130-2	Sequence 2, Appli
56	109.5	1.7	7968	13	US-10-077-130-5	Sequence 5, Appli
57	109	1.7	2845	13	US-10-267-502-372	Sequence 372, App
58	108	1.7	386	12	US-10-424-599-250597	Sequence 250597,
59	108	1.7	499	15	US-10-369-493-10577	Sequence 10577, A
60	108	1.7	2596	14	US-10-307-019-6	Sequence 6, Appli
61	107.5	1.7	8026	12	US-10-132-134-12	Sequence 12, Appl
62	107	1.7	905	15	US-10-369-493-2550	Sequence 2550, Ap
63	107	1.7	1279	12	US-10-332-288-6	Sequence 6, Appli
64	106.5	1.7	1299	14	US-10-156-761-12449	Sequence 12449, A
65	106.5	1.7	2448	12	US-10-210-172-48	Sequence 48, Appl
66	106.5	1.7	3298	12	US-10-210-172-50	Sequence 50, Appl
67	106.5	1.7	3298	14	US-10-160-758-16	Sequence 16, Appl
68	106.5	1.7	3298	14	US-10-174-677-8	Sequence 8, Appli
69	105.5	1.7	707	14	US-10-120-801-51	Sequence 51, Appl
70	105.5	1.7	1062	15	US-10-156-761-9979	Sequence 9979, Ap
71	105.5	1.7	1563	16	US-10-389-566-608	Sequence 608, App
72	105.5	1.7	1967	15	US-10-334-143-34	Sequence 34, Appl
73	105.5	1.7	1967	14	US-10-219-834-85	Sequence 85, Appl
74	105.5	1.7	1967	14	US-10-225-567A-575	Sequence 575, App
75	104.5	1.7	635	10	US-10-851-847-5	Sequence 5, Appli
76	104.5	1.7	635	16	US-10-643-233-5	Sequence 5, Appli
77	104.5	1.7	1471	8	US-08-811-519A-1	Sequence 1, Appli
78	104.5	1.7	1515	12	US-10-240-154-8	Sequence 8, Appli
79	104.5	1.7	3530	12	US-10-296-115-1101	Sequence 1101, Ap
80	104.5	1.7	6304	14	US-10-147-026-16	Sequence 16, Appl
81	104	1.7	3192	12	US-10-132-134-10	Sequence 10, Appl
82	103.5	1.6	495	12	US-10-425-114-65528	Sequence 65528, A
83	103.5	1.6	942	12	US-10-282-122A-57721	Sequence 57721, A
84	103.5	1.6	1750	12	US-10-243-552-920	Sequence 920, App
85	103	1.6	1050	12	US-10-282-122A-78119	Sequence 78119, A
86	103	1.6	3472	13	US-10-027-806-4	Sequence 4, Appli
87	103	1.6	3472	13	US-10-034-623-4	Sequence 4, Appli
88	103	1.6	3472	14	US-10-027-801-4	Sequence 4, Appli

```
89   103    1.6  US-10-029-120-4        14  3472  Sequence 4, Appli
90   102    1.6  US-10-288-122A-47996   12  625   Sequence 47996, A
91   102    1.6  US-10-282-122A-62122   12  876   Sequence 62122, A
92   102    1.6  US-10-369-493-359      15  1074  Sequence 359, App
93   102    1.6  US-09-970-944-21       11  4590  Sequence 21, Appl
94   102    1.6  US-10-160-758-13       14  4590  Sequence 13, Appl
95   102    1.6  US-10-160-758-14       14  4590  Sequence 14, Appl
96   102    1.6  US-10-060-036-157      14  4590  Sequence 157, App
97   102    1.6  US-10-295-027-1323     15  4590  Sequence 1323, Ap
98   101.5  1.6  US-10-128-714-8088     14  1028  Sequence 8088, Ap
99   101    1.6  US-10-425-114-70947    12  336   Sequence 70947, A
100  101    1.6  US-10-282-122A-50633   12  587   Sequence 50633, A
```

ALIGNMENTS

RESULT 1
US-09-769-699-2
; Sequence 2, Application US/09769699
; Publication No. US20010039051A1
; GENERAL INFORMATION:
; APPLICANT: Silverstein, Saul J
; APPLICANT: Lungu, Octavian
; APPLICANT: Gershon, Anne A
; APPLICANT: Annunziato, Paula W
; TITLE OF INVENTION: VZV ORF29p Protein-Related Compositions and Methods
; FILE REFERENCE: 0575/61152-A
; CURRENT APPLICATION NUMBER: US/09/769,699
; CURRENT FILING DATE: 2002-04-22
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
;
; SEQ ID NO 2
; LENGTH: 1203
; TYPE: PRT
; ORGANISM: Varicella zoster
US-09-769-699-2

```
Query Match          100.0%;   Score 6294;  DB 12;  Length 1203;
Best Local Similarity 100.0%;  Pred. No. 0;
Matches 1203;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1  MENTQKTVTVPTGPLGVYVACRVEDLDLEBISFLAARSTDSDLALLPLMRNLTVEKTFTS   60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  MENTQKTVTVPTGPLGVYVACRVEDLDLEBISFLAARSTDSDLALLPLMRNLTVEKTFTS   60

Qy   61  SLAVVSGARTTGLAGAGITLKLTTSHFYPSVFVFHGGKHVLPSSAAPNLTRACNAARERF  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  SLAVVSGARTTGLAGAGITLKLTTSHFYPSVFVFHGGKHVLPSSAAPNLTRACNAARERF  120

Qy  121  GFSRCQGPPVDGAVETTGAEICTRLGLEPENTILYLVVTALFKEAVFMCNVFLHYGGLDI  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  GFSRCQGPPVDGAVETTGAEICTRLGLEPENTILYLVVTALFKEAVFMCNVFLHYGGLDI  180

Qy  181  VHINHGDVIRIPLFPVQLFMPDVNRLVPDPFNTHHRSIGEGFVYPTPFYNTGLCHLIHDC  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  VHINHGDVIRIPLFPVQLFMPDVNRLVPDPFNTHHRSIGEGFVYPTPFYNTGLCHLIHDC  240

Qy  241  VIAPMAVALRVRNVTAVARGAAHLAFDENHBGAVLPPDITYTYFQSSSSGTTTARGARRN  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  VIAPMAVALRVRNVTAVARGAAHLAFDENHBGAVLPPDITYTYFQSSSSGTTTARGARRN  300

Qy  301  DVNSTSKPSPSGGFERRLASIMAADTALHAEVIFNTGIYEBTPTDIKEWPMFIGMEGTLP  360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301  DVNSTSKPSPSGGFERRLASIMAADTALHAEVIFNTGIYEBTPTDIKEWPMFIGMEGTLP  360

Qy  361  RLNALGSYTARVAGVIGAMVFSPNSALYLTEVEDSGMTEAKDGGPGSFNRFYQFAGPHL   420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361  RLNALGSYTARVAGVIGAMVFSPNSALYLTEVEDSGMTEAKDGGPGSFNRFYQFAGPHL   420

Qy  421  AANPQTDRDGHVLSSQSTGSSNTEFSVDYLALICGFGAPLLARLLFYLERCDAGAFTGGH  480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421  AANPQTDRDGHVLSSQSTGSSNTEFSVDYLALICGFGAPLLARLLFYLERCDAGAFTGGH  480

Qy  481  GDALKYVTGTFDSEIPCSLCKGHTRPVCAHTTVHRLRQRMPRFGQATRQPIGVFGTMNSQ  540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481  GDALKYVTGTFDSEIPCSLCKGHTRPVCAHTTVHRLRQRMPRFGQATRQPIGVFGTMNSQ  540

Qy  541  YSDCDPLGNYAPYLILRKPGDQTEAAKATMQDTYRATLERLFIDLEQERLLDRGAPCSSE  600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541  YSDCDPLGNYAPYLILRKPGDQTEAAKATMQDTYRATLERLFIDLEQERLLDRGAPCSSE  600

Qy  601  GLSSVIVDHPTFRRILDTLRARIEQTTTQFMKVLVETRDYKIREGLSEATHSMALTFDPY  660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601  GLSSVIVDHPTFRRILDTLRARIEQTTTQFMKVLVETRDYKIREGLSEATHSMALTFDPY  660

Qy  661  SGAFCPITNFLVKRTHLAVVQDLALSQCHCVFYGQQVEGRNFRNQFQPVLRRRFVDLFNG  720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661  SGAFCPITNFLVKRTHLAVVQDLALSQCHCVFYGQQVEGRNFRNQFQPVLRRRFVDLFNG  720

Qy  721  GFISTRSITVTLSEGPVSAPNPTLGQDAPAGRTFDGDLARVSVEVIRDIRVKNRVVFSGN  780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  721  GFISTRSITVTLSEGPVSAPNPTLGQDAPAGRTFDGDLARVSVEVIRDIRVKNRVVFSGN  780

Qy  781  CTNLSEARARARIVGLASAYQRQEKRVDMLHGALGFLLKQFHGLLFPRGMPPNSKSPNPQW  840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781  CTNLSEARARARIVGLASAYQRQEKRVDMLHGALGFLLKQFHGLLFPRGMPPNSKSPNPQW  840

Qy  841  FWTLLQRNQMPADKLTHEITTIAAVKRFTEBYAAINFINLPPTCIGELAQFYMANLILK   900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  841  FWTLLQRNQMPADKLTHEITTIAAVKRFTEBYAAINFINLPPTCIGELAQFYMANLILK   900

Qy  901  YCDHSQYLINTLTSIITGARRPRDPSSVLHWIRKDVTSAADIETQAKALLEKTENLPELW  960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  901  YCDHSQYLINTLTSIITGARRPRDPSSVLHWIRKDVTSAADIETQAKALLEKTENLPELW  960

Qy  961  TTAFTSTHLVRAAMNQRPMVVLGISISKYHGAAGNNRVFQAGNWSGLNGGKNVCPLFTFD 1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  961  TTAFTSTHLVRAAMNQRPMVVLGISISKYHGAAGNNRVFQAGNWSGLNGGKNVCPLFTFD 1020

Qy 1021  RTRRFIIACPRGGFICPVTGPSSGNRETTLSDQVRGIIVSGGAMVQLAIYATVVRAVGAR 1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021  RTRRFIIACPRGGFICPVTGPSSGNRETTLSDQVRGIIVSGGAMVQLAIYATVVRAVGAR 1080

Qy 1081  AQHMAFDDWLSLTDDBFLARDLELHDQIIQTLETPWTVEGALEAVKILDEKTAGDGET   1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1081  AQHMAFDDWLSLTDDBFLARDLELHDQIIQTLETPWTVEGALEAVKILDEKTAGDGET   1140

Qy 1141  PTNLAFNFDSCEPSHDTTSNVLNISGSNISGSTVPGLKRPPEDDELFDLSGIPIKHGNIT 1200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1141  PTNLAFNFDSCEPSHDTTSNVLNISGSNISGSTVPGLKRPPEDDELFDLSGIPIKHGNIT 1200

Qy 1201  MEM 1203
         |||
Db 1201  MEM 1203
```

RESULT 2
US-10-050-673-2
; Sequence 2, Application US/10050673
; Publication No. US20020151033A1
; GENERAL INFORMATION:
; APPLICANT: David M. Knipe
; APPLICANT: Travis J. Taylor
; APPLICANT: Elizabeth McNamee
; TITLE OF INVENTION: Replication-Competent Virus Expressing A
; TITLE OF INVENTION: Fusion Protein
; FILE REFERENCE: HU98-05
; CURRENT APPLICATION NUMBER: US/10/050,673
; CURRENT FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: US/09/127,227
; PRIOR FILING DATE: 1998-07-31
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 3.0
;
; SEQ ID NO 2
; LENGTH: 1452

```
;  TYPE: PRT
;  ORGANISM: herpesvirus
US-10-050-673-2

Query Match     48.5%;    Score 3054;  DB 13;  Length 1452;
Best Local Similarity  49.8%;  Pred. No. 5e-294;
Matches  609;  Conservative 200;  Mismatches 366;  Indels 48;  Gaps 17;

Qy    1  MENTQKTVT---VPTGPLGYVY--ACRVEDLLDEEISFLAARSTDSDLALLPLMRNLTVE    55
Db    1  METKPKIATTIKVPPGPLGYVYARACPSEGIEL--LALLSARSGDADVAVAPLVVGLTVE    58

Qy   56  KTFTSSLAVVSGARTTGLAGAGITLKLTTSHPYPSVVFHGGKHVLPSSAAPNLTRACNA   115
Db   59  SGFEANVAVVVGSRTTGLGGTAVSLKLITPSHYSSSVVFHGGRHLDPSTQAPNLTRLCER   118

Qy  116  ARERRFGFSRCQGPPVDGAVETGAEICTRLGLEPENTILYLVVTALFKEAVFMCNVFLHY   175
Db  119  ARRHFGFSDYTPRPGDLKHETTGEALCERLGLDPDRALLYLVVTEGFKEAVCINNTFLHL   178

Qy  176  GGLDIVIHINHGDVIRIPLFPVQLFMPDVNRLVPDPFNTHHRSIGEGFVYPTPFYNTGLCH   235
Db  179  GGSDKVTIGGABVHRIPVYPLQLFMDFSRVIAEPFNANHRSIGENFTYPLPFFNRPLNR   238

Qy  236  LIHDCVIAPMAVALRVRNVTAVARGAAHLAPDENHEGAVLPPDITYYFQSSSSGTTTAR   295
Db  239  LLFEAVVGPAAVALRCRNVDAVARAAAHLAFDENHEGAALPADITFTAFEASQG--KTPR   296

Qy  296  GARRNDVNSTSKPSPSGFERRLASIMAADTALHAEVIFNTGIYEETPTDIKEWPMFIGM   355
Db  297  GGR-----DGGGKGPAGGFEQRLASVNAGDAALALESIVSMAVFDEPPTDISAWPLCEGQ   351

Qy  356  EGTLPRLNALGSYTARVAGVIGAMVFSPNSALYLTEVEDSGMTEAKDGGPGPSFNRFYQF   415
Db  352  DTAAAARANAVGAYLARAAGLVGAMVFSTNSALHLTEVDDAGPADPKDHSK-PSFYRFFLV   410

Qy  416  AGPHLAANPQTDRDGHVL------SSQSTGSSNTEFSVDYLALICGFGAPLLARLLFYL   468
Db  411  PGTHVAANPQVDREGHVVPGFEGRPTAPLVGGTQ-EFAGEHLAMLCGFSPALLAKMLFYL   469

Qy  469  ERCDAGAFTGGHG-DALKYVTGTFDSEIPCSLCEKHTRPVCAHTTVHRLRQRMPRFGQAT   527
Db  470  ERCDGGVIVGRQEMDVFRYVADSNQTDVPCNLCTFPDTRHACVHTTLMRLRARHPKFASAA   529

Qy  528  RQPIGVFGTMNSCYSDCDPLGNYAPYILILRKPGDQTEAAKATMQDTYRATLERLFIDLEQ   587
Db  530  RGAIGVFGMNSMYSDCDVLGNYAAFSALKR-ADGSETARTIMQETYRAATERVMAELET   588

Qy  588  ERLLDRGAPCSSEGLSSVIVDHPTFRRILDTLRARIEQTTTQFMKVLVETRDYKIREGLS   647
Db  589  LQYVDQAVPTAMGRLETIITNRRALHTVVNNVRQVVDREVEQLMRNLVEGRNFKFRDGLG   648

Qy  648  EATHSMALTFDPYSGACFPITNFLVKRTHLAVVQDLALSQCHCVFYGQQVEGRNFRNQFQ   707
Db  649  EANHAMSLTLDPYACGPCPLLQLLGRRSNLAVVQDLALSQCHGVFAGQSVEGRNFRNQFQ   708

Qy  708  PVLRRFVDLLFNGGFISTRSITVTLSEG-PVSAPNPTLGQDAPAGRTFDGDLARVSVEVI   766
Db  709  PVLRRRVMDMFNNGFLSAKTLTVALSEGAAICAPSLTAGOTPAESSFEGDVARVTLGFP   768

Qy  767  RDIRVRVFSGNCTNLSEAARARLVGLASAYQRQBKRVDMLHGALGFLLKQFHGLLFP   826
Db  769  KELRVKSRVLFAGASANASEAAKARVASLQSAYQKPDKRVDILLGPLGFLLKQFHAAIFP   828

Qy  827  RGMPPNSKKSPNPQWFWTLLQRNQMPADKLTHEEITTIAAVKRFTEEYAAINFINLPPTCI   886
Db  829  NGKPPGSNQPNPQWFWTALQRNQLPARLLSREDIETIAFIKKFSLDYGAINFINLAPNNV   888

Qy  887  GELAQFYMANLILKYCDHSQYLINTLTSIITGARRRPDPSSVLHWIRKDVTSAADIETQA   946
Db  889  SELAMYYMANQILRYCDHSTYFINTLAIIAGSRRPSVQAAAAW---SAQQGAGLERAGA   945

Qy  947  KALLLEKTENLPELWTTAFTSTHLVRAAMNQRPMVLGISISKYTHGAAGNNRVFQAGNWSG  1006
Db  946  RALMDAVDAHPGAWTSMFASCNLLRPVMAARPMVLGLSISKYYGMAGNDRVFQAGNWAS   1005

Qy 1007  LNGGKNVCPLFTPDRTRRPIIACPRGGFICPVTGPSSGGNRETTLSDQVRGIIVSGGAMVQ  1066
Db 1006  LMGGKNACPLLIFDRTRKFVLACPRAGFVCAASNLGGGAHESSLCEQLRGLIISEGGAAVA  1065

Qy 1067  LAIYATVRAVGARAQHMAFPDWLSLTDDEFLARDLEELHDQIIQTLETPWTVEGAL---   1123
Db 1066  SSVFVATVKSLGPRTQQLQIEDWLALLEDEYLSEEMMELTARALERGNGEWSTDAALEVA  1125

Qy 1124  -EAVKILDEKTTAGDGETPINLAFNFD--SCEPSHDTTSNVLNISGSNISGSTVPGLKRP  1180
Db 1126  HEAEALVSQLGNAGE-------VFNFGDFGCE------DDNATPFGGPGAPGPAFAGRKRA  1173

Qy 1181  PEDDELFDLSGIPIKHGNITMEM  1203
Db 1174  FHGDDPFG-EGPPDKKGDLTLDM  1195


RESULT 3
US-10-200-562-200
; Sequence 200, Application US/10200562
; Publication No. US20030165819A1
; GENERAL INFORMATION:
; APPLICANT: McGowen, Patrick
; APPLICANT: Hosken, Nancy A.
; TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION:  TREATMENT OF HERPES SIMPLEX VIRUS INFECTION
; FILE REFERENCE: 210121.538C2
; CURRENT APPLICATION NUMBER: US/10/200,562
; CURRENT FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 200
;    LENGTH: 1196
;    TYPE: PRT
;    ORGANISM: HSV2
US-10-200-562-200

Query Match     47.9%;    Score 3015.5;  DB 14;  Length 1196;
Best Local Similarity  49.0%;  Pred. No. 2.5e-290;
Matches  595;  Conservative 213;  Mismatches 366;  Indels 41;  Gaps 16;

Qy    4  TQKTVTVPTGPLGYV---ACRVEDLLDEEISFLAARSTDSDLALLPLMRNLTVEKFTSS    61
Db    7  TTTTVKVPPGPMGYVVGRACPAEGLEL--LSLLSARSGDADVAVAPLIVGLTVESGPEAN    64

Qy   62  LAVVSGARTTGLAGAGITLKLTTSHFYPSVVFVFHGGGHVLPSSAAPNLTRACNAARERFG   121
Db   65  VAAVVGSRTTGLGGTAVSLKLMPSHYSPSVVFVFHGGRHLAPSTQAPNLTRLCERARPHFG   124

Qy  122  FSRCQGPPVDGAVETGAEICTRLGLEPENTILYLVVTALFKEAVFMCNVPLHYGGLDIV   181
Db  125  FADYARPCDLKHETTGDALCERLGLDPDRALLYLVVTEGFREAVCISNTFLHLGGMDKV   184

Qy  182  HINHGDVIRIPLFPVQLFMPDVNRLVPDPFNTHHRSIGEGFVYPTPFYNTGLCHLIHDCV   241
Db  185  TIGDAEVHRIPVYPLQMFMPDFSRVIADPFFNCNHRSIGENFNYPLPFFNRPLARLLFEAV   244

Qy  242  IAPMAVALRVRNVTAVARGAAHLAPDENHEGAVLPPDITYYFQSSSSGTTTARGARRND   301
Db  245  VGPAAVALRARNVDAVARAAAHLAFDENHEGAALPADITFTAFEASQG--KPQRGAR--   299

Qy  302  VNSTSKPSPSGFERRLASIMAADTALHAEVIFNTGIYEETPTDIKEWPMFIGMEGTLPR   361
Db  300  --DAGNKGPAGGFEQRLASVNAGDAALALESIVSMAVFDEPPDITTWPLLEGQETPAAR   357

Qy  362  LNALGSYTARVAGVIGAMVFSPNSALYLTEVEDSGMTEAKDGGPGPSFNRFYQFAGPHLA   421
Db  358  AGAVGAYLARAAGLVGAMVFSTNSALHLTEVDDAGPADPADPKDHSK-PSFYRFFLVPGTHVA   416

Qy  422  ANPQTDRDGHVL-------SSQSTGSSNTEFSVDYLALICGFGAPLLARLLFYLERCDAG   474
```

```
; TYPE: PRT
; ORGANISM: HSV2
US-10-237-551-200

Query Match         47.9%;  Score 3015.5;  DB 14;  Length 1196;
Best Local Similarity   49.0%;  Pred. No. 2.5e-290;
Matches  595;  Conservative 213;  Mismatches 366;  Indels 41;  Gaps 16;

Qy    4 TQKTVTVTPTGPLGYVY--ACRVEDLDEEISFLAARSTDSDIALLPLMRNLIVEKTFTSS   61
         |||: :|| ||| ||||:   :: :  ::|:|  ||| :||: : :  :|  : ||:|:|
Db    7 TTTTVKVPPGPMGYVYGRACPAEGLEL--LSLLSARSGDADVAVAPIIVGLIVESGFEAN   64

Qy   62 LAVVSGARTTGLAGAGITLKLTTSHFYPSVFVPHGGKHVLPSSAAPNLTRACNAARERFG  121
         :|:| |:|||||.|:|: ||| .||:.|||: |||| |: || ||||||| |: ||. ||
Db   65 VAAVVGSRTTGLGGTAVSLKLMPSHYSPSVVYPHGGRHLAPSTQAPNLTRLCERARPHFG  124

Qy  122 FSRCQGPPVDGAVETTGABICTRLGLEPENTILYLVVTALFKEAVFMCNVFLHYGGLDIV  181
         |:  |  | |   ETTG |:| ||||.| | :|||| || |:||| |:|| ||||:| |
Db  125 FADYAPRPCDLKHETTGDALCERLGLDPRALLYLVITEGFREAVCISNTFLHLGGMDKV   184

Qy  182 HINHGDVIRIPLFPVQLFMPDVNRLVPDPFNTHHRSIGEGFVVPTPPYNTGLCHLIHDCV  241
         .|. .|||||: ||||:||||:.|:| ||||.:||||| || |  | |  | ||: |: |
Db  185 TIGDAEVHRIPVVPLQWFMPDFSRVIADPFNCNHRSIGENFNYPLPFNRPLARLLFEAV   244

Qy  242 IAPMAVALRVRNVTAVARGAAHLAFDENHEGAVLPPDITYTYFQSSSSGTTARGARRND   301
          .|:||||| ||| |||| ||||||||||||| || ||| | | ||::   ||| |
Db  245 VGPAAVALRARNVDAVARAAAHLAFDENHEGAALPADITFTAFABASQG--KPQRGAR--  299

Qy  302 VNSTSKPSPSGGFERRLASIMADTALHAEVIFNTGIYBETPTDIKEWPMFIGMEGTLPR  361
           . .  .| ||||:|||| ||  ||| | || ||:  |::  || |: ||| : |::
Db  300 --DAGNKGPAGGFEQRLASVMAGDAALALESIVSMAVFDEPPDITTWPLLEGQETPAAR  357

Qy  362 LNALGSYTARVAGVIGAMVFSPNSALYLTEVEDSGMTEAKDGGPGPSNRPYQFAGPHLA  421
           |:|:| || ||::||||||.||||:|||| |:| .  :||:  ::  .:|  ||.||
Db  358 AGAVGAYLARAAGLVGAMVFSTNSALHLTEVDDAGPADPKDHSK-PSFYRFFLVPGTHVA  416

Qy  422 ANPQTDRDGHVL------SSQSTGSSNTBFSVDYLALICGFGAPLLARLLFYLERCDAG  474
         ||||.:|:||| |       :: | |:  ||   : | ||| ||||:::||||||||.|
Db  417 ANPQLDREGHVVPGYEGRPTAPLVGGTQ-EFAGEHLAMLCGFSPALLAKMLFYLERCDGG  475

Qy  475 AFTGHG-DALKYVTGTFDSEIPCSLCEKHTRPVCAHTTVHRLQRMPRFGQATRQPIGV  533
          .:|||  |||||| ::||||||:||: :|: ||||||::||:|: ||. ::||:||
Db  476 VIVGRQEMDVFRYVADSGQTDVPCNLCTFETRHACAHTTLMRLRARHPKFASAARGAIGV  535

Qy  534 FGTMNSQYSDCDPLGNYAPYLILRKPGDQTEAAKATMQDTYRATLERLFIDLEQERLLDR  593
         |||||| ||||| |||||  : | || |  :  ::||:|||| |||: : : |:|| : :
Db  536 FGTMNSAYSDCDVLGNYAAFSALKR-ADGSENTRTIMQETYRAATERVMAELEALQYVDQ  594

Qy  594 GAPCSSEGLSSVIVDHPTFRRILDTLRARIEQTTQFMKVLVETRDYKIREGLSEATHSM  653
          |.  | |:||:||::| ::   : :  :|.:  :::  |:: |:: :|:||:||.|||
Db  595 AVPTALGRLETIIGNREALHTVVNNIKQLVDREVEQLMRNLIEGRNFKFRDGLAEANHAM  654

Qy  654 ALTFDPYSGAFCPIITNFLVKRTHLAVVQDLALSQCHCVFYGQQVEBGRNFRNQFQPVLRRR  713
         :|: |||: | ||:  ::  :::.||:||||||||| |||.|.|| ||||||||||||||
Db  655 SLSLDPYTCGPCPLLQLLARRSNLAVYQDLALSQCHGVFAGQSVEGRNFRNQFQPVLRRR  714

Qy  714 FVDLFNGGFISTRSITVTLSEG-PVSAPNPTLGQDAPAGRTFDGDLARVSVEVIRDIRVK  772
         .:||||.||:| ::||| |||| .: ||:.| ||:|| |:  | |:||| : : :|:|||
Db  715 VMDLFNNGFLSAKTLTVALSEGAAICAPSLTAGQTAPAESSFEGDVARVTLGFPKELRVK  774

Qy  773 NRVVFSGNCTNLSEAARARLVGLASAYQREKRVDMLHGALGFLLKQFHGLLFPRGMPPN  832
          ||:|:|.: | :||| || ||:|:||::  ||| | | |||||||||.::||.| ||
Db  775 SRVLFAGASANASEAAKARVASLQSAYQKPDKRVDILLGPLGFLLKQFHAVIFPNGKPPG  834

Qy  833 SKSPNPQWFWTLLQRNQMPADKLTHEEITTIAAVKRFTEEYAAINFINLPPTCIGELAQF  892
          : ||||||||::|||:.||: |:|||||:||: |||:  |.||||||: :.: ||::
Db  835 SNQPNPQWFWTALQRNQLPARLLSREDIETIAFIKRFSLLDYGAINFINLAPNNVSELAMY  894

Qy  893 YMANLILKYCDHSQYLINTLTSIITGARRPRDPSSVLHWIRKDVTSAADIETQAKALLEK  952
         ||||:||:|||||:|:|||||::|:| :||:  ||: .  :  ::::| |: :||||:
Db  895 YMANQILRYCDHSTYFINTLTAVIAGSRRPPSVQAAAAWAPQ---GGAGLEAGARALMDS  951

Qy  953 TENLPELWTTAFTSTHLVRAAMNQRPMVVLGISISKYHGAAGNNRVFQAGNWSGLNGGKN 1012
         .: ||: |::  ::  :|:|||:|||||||||:|||||:||.|:||||||||:||:||||
Db  952 LDAHPGAWTSMFASCNLLRPVMAARPMVVLGLSISKYYGMAGNDRVFQAGNWASLLGGKN 1011

Qy 1013 VCPLFTFPDRTRRFIIACPRGGFICPVTGPSSGNRETTLSDQVRGIIVSGGAMVQLAIYAT 1072
         .|||: |||||:||::||||.||:| .:  |.|::  .|:|:|||||: |||.| :: :.
Db 1012 ACPLLIFDRTRKFVLACPRAGFVCAASSLGGGAHEHSLCEQLRGIIAEGGAAVASSVFVA 1071

Qy 1073 VVRAVGARAQHMAFDDWLSLTDDEFLARDLEELHDQIIQTLETPWTVEGAL---EAVKI 1128
          |:::|.|::::  ::||:| :||:|: : :| :: ::  :: : : :  :   :|| |
Db 1072 TVKSLGPRTQQLQIEDWLALLEDEYLSEEMMEFTTRALERGHGEWSTDAALEVAHEABAL 1131

Qy 1129 LDEKTAGDGETPTNLAFNFDSCEPSHDTTSNVLNISGSNISGSTVPGLKRPBEDDELFD 1188
           : .: ::|    || |||    : : :  :: :|: |:          :: :|: ||
Db 1132 VSQLGAAGE------VFNFGDFGDEDDHAASFGGLAAA--AGAAGVARKRAFHGDDDPFG 1182

Qy 1189 LSGIPIKHGNITMEM 1203
         ||:        ||:|
Db 1183 -EGPPEKK-DLTLDM 1195
```

RESULT 4
US-10-237-551-200
; Sequence 200, Application US/10237551
; Publication No. US20030165820A1
; GENERAL INFORMATION:
; APPLICANT: Day, Craig H.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Parsons, Joseph M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF HERPES SIMPLEX VIRUS INFECTION
; FILE REFERENCE: 210121.538C3
; CURRENT APPLICATION NUMBER: US/10/237,551
; CURRENT FILING DATE: 2002-09-06
; NUMBER OF SEQ ID NOS: 254
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 200
; LENGTH: 1196

Qy   422 ANPQTDRDGHVL------SSQSTGSSNTEFSVDYLALICGFGAPLLARLLFYLERCDAG 474
          |||:||::|:   :: :::|:::||||||
Db   417 ANPQLDREGHVVPGYEGRPTAPLVGGTQ-EFAGEHLAMLCGFSPALLAKMLFYLERCDGG 475

Qy   475 AFTGHG-DALKYVTGFPDSEIPCSLCEKHTRPVCAHTTVHRLRQRMRPFGQATRQPIGV 533
          | :::   ::|:|||||||| ::|: |::   :|||||:|||
Db   476 VIVRQEMDVFRRYVADSGQTDVPCNLCTFETRHACAHTTLMRLRARHPKFASAARGAIGV 535

Qy   534 FGTMNSQYSDCDPLGNYAPYLILRKPGDQTEAAKATMQDTYRATLERLFIDLEQERLLDR 593
          |||||||:||| ||||| : |||||| : ||| |||||||||| |||||||||
Db   536 FGTMNSAYSDCDVLGNYAAFSALKR-ADGSENTRTIMQETYRAATERVWAELALQYVDQ 594

Qy   594 GAPCSSEGLGSSVIVDHPTPRRILDTLRARIEQTTQFMKVLVETRDYKIREGLSEATHSM 653
          || |:| :|||| |||||| |||||| |||| ||| |:||::||:||
Db   595 AVFTALGRLETIIGNREALHTVNNIKQLVDREVEQLMRNLIEGRNFKFRDGLAEANHAM 654

Qy   654 ALTFDPYSGAFCPITNFLVKRTHLAVVQDLALSQCHCVFYGQQVEGRNFRNQFQPVLRRR 713
          ||||||:| | ::||||| :|:||| : |::: | :||||:||:|||||||||
Db   655 SLSLDPYTCGPCPLLQLLARRSNLAVYQDLALSQCHGVPAGQSVEGRNFRNQFQPVLRRR 714

Qy   714 FVDLFNGGFPISTRSITVILSEG-PVSANPTLGQDAPAGRTFPGDLARVSVEVIRDIRVK 772
          |:|||| | ||:|||||||| | ||||| || ||||| || |:|||:|||||
Db   715 VMDLFNNGFLSAKTLTVALSEGAAICAPSLTAGQTAPAESSFEGDVARVTLGFPKELRVK 774

Qy   773 NRVVFSGNCTNLSEAARARLVGLASAYQREKRVDMLHGALGFLLKQFHGLLPPRGMPPN 832
          |:| :|: :::|||:||||| : ::::|| ||| |:||||||||||||||||||
Db   775 SRVLFAGASANASEAAKARVASLQSAYQKPDKRVDILLGPLGFLLKQFHAVIFNGKPPG 834

Qy   833 SKSPNPQWFWTLLQRNQMPADKLTHEEITTIAAVKRFTEEYAAINFINLPPTCIGELAQF 892
          :||||||||||||| |:||||||||:|: |:|| |||| |||:|||| :
Db   835 SNQPNPQWFWTALQRNQLPARLLSREDIETIAFIKRFSLDYGAINFINLAPNNVSELAMY 894

Qy   893 YMANLILKYCDHSQYLINTLTSIITGARRPRDPSSVLHWIRKDVTSAADIETQAKALLEK 952
          |||| :||||||||||||| |:| |:||:| | | :| :|| ||
Db   895 YMANQILRYCDHSTYFINLTAVIAGSRRPPSVQAAAAWAPQ--GGAGLEAGARALMDS 951

Qy   953 TENLPELWTTAFTSTHLVRAAMNQRPMVLGISISKYHGAAGNNRVFQAGNWSGLNGGKN 1012
          |:| | |||:|||| |:|||||||||| | || || | ||:||:|||||| |:|| |||||
Db   952 LDAHPGAWTSMFASCNLLRPVMAARPMVVLGLSISKYGMAGNDRVFQAGNWASLLGGKN 1011

Qy 1013 VCPLFTFDRTRRFIIACPRGGFICPVTGPSSGNRETTLSDQVRGIIVSGGAMVQLAIYAT 1072
          |||||||||||||||||||||| ||||||||||||||||||||||||||:||||||||||
Db 1012 ACPLLIFDRTRKFVLACPRAGFVCAASSLGGAHEHSLCEQLRGIIAEGGAAVASSVFVA 1071

Qy 1073 VVRAVGARAQHMAFPDWLSLTDDEFLARDLEELHDQIIQTLETPWTVEGAL----EAVKI 1128
          |::| | |:|| |:||:||:|:||| |:| | || | |:||||
Db 1072 TVKSLGPRTQQLQIEDWLALLEDEYLSEEMMEFTTRALERGHGEWSTDAALEVAHEAEAL 1131

Qy 1129 LDEKTTAGDGETPTNLAFNFDSCEPSHDTTSNVLNISGSNISGSTVPGLKRPEDDELFD 1188
          |||||||||||||||||||||||| :::|||||:||||||||||:||||||||||||
Db 1132 VSQLGAAGE------VFNFGFDGEDDHAASFGGLAAA--AGAAGVARKRAFHGDDDPFG 1182

Qy 1189 LSGIPIKHGNITMEM 1203
          ||||||||| :||:|
Db 1183 -EGPPEKK-DLTLDM 1195

RESULT 5
US-10-237-551-232
; Sequence 232, Application US/10237551
; Publication No. US20030165820A1
GENERAL INFORMATION:
; APPLICANT: Day, Craig H.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Parsons, Joseph M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF HERPES SIMPLEX VIRUS INFECTION
; FILE REFERENCE: 210121.538C3
; CURRENT APPLICATION NUMBER: US/10/237,551
; CURRENT FILING DATE: 2002-09-06
; NUMBER OF SEQ ID NOS: 254
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 232
; LENGTH: 1196
; TYPE: PRT
; ORGANISM: Herpes simplex virus
US-10-237-551-232

Query Match   47.9%; Score 3015.5; DB 14; Length 1196;
Best Local Similarity 49.0%; Pred. No. 2.5e-290;
Matches   595; Conservative 213; Mismatches 366; Indels 41; Gaps 16;

Qy   4 TQKTVTVPTGPLGYVY--ACRVEDLDLEISFLAARSTDSDLALLPLMRNLTVEKTFTSS   61
          | :::|:|||||| | |::| |::| :   :||:|||||| :|: : ::
Db   7 TTTVKVPPGPMGYYVGRACPAEGLEL--LSLLGARSGDAVVAPLIVGLTVTVESGFEAN   64

Qy   62 LAVVSGARTGLAGAGITLKLTTSHFYPSVFVFHGGKHVLPSSAAPNLTRACNAARERFG 121
          || :|| | |||| |:|:| |||||||: ||| | :| |||:| |: || ||
Db   65 VAAVVGSRTTGLGGTAVSLKLMPSHYSPSVYVFHGGRHLAPSTQAPNLTRLCERARPHG 124

Qy   122 FSRCCQGPPVDGAVETTGAEICTRLGLGEPENTILYLVVTALFKEAVFMCNVPLHYGGLDIV 181
          | : ||| | ||| | |||| ||:||||| :|::|| | | ||||||||:|
Db   125 FADYAPRPCDLKHETTGDALCERLGLGDPDRALLYLVITEGFREAVCISNTFLHLGGMDKV 184

Qy   182 HINHGDVIRIPLFPVQLFMPDVNRLVPDPNTHHRSIGEGFVPTPFYNTGLCHLIHDCV 241
          ||: || | | ||| :|| || :|: | :| ||||:||||| |||| || ||
Db   185 TIGDAEVHRIPVYPLQMFMPDFSRVIADPFNCNHRSIGENFNYPLPFFNRPLARILFEAV 244

Qy   242 IAPMAVALRVRNVTAVARGAAHLAPDENHEGAVLPPDITVTYFQSSSSGTTTARGARRND 301
          || |||| | | ||| || |||| ||||||| |||||||||| :: |:: | | ||
Db   245 VGPAAVALRARNVDAVARAAAHLAPDENHEGAALPADITTAFFEASQG--KPQRGAR--- 299

Qy   302 VNSTSKPSPSGFERRLASIMAADTALHAEVIFNTGIYEETPTDIKEWPMFIGMEGTLPR 361
          | :| | ||| ||||| | | ||| | : |:||||||||||| |: | ||||
Db   300 --DAGNKGPAGGFEQRLASVMAGDAALALESIVSMAVFDEPPPDITTWPLLEGQETPAAR 357

Qy   362 LNALGSYTARVAGVIGAMVFSPNSALYLTEVEDSGMTEAKDGGFGPSFNRFYQPAGPHLA 421
          || || | | | |||| :|| ::|||:|||| |: :|:|| | ::|| |||| |:
Db   358 AGAVGAYLARAAGLVGAMVFSTNSALHLTEVDDAGPADPKDHSK-PSFYRFFLPVPGTHVA 416

```
;   LENGTH: 274
;   TYPE: PRT
;   ORGANISM: Herpes simplex virus
US-10-237-551-231

Query Match          12.5%;    Score 788;   DB 14;   Length 274;
Best Local Similarity 56.5%;    Pred. No. 3.1e-69;
Matches 153;   Conservative  41;   Mismatches  75;   Indels  2;   Gaps  1;

Qy     28  LEEISFLAARSTDSDLALLPLMRNLTVEKTFTSSLAVVSGARTTGLAGAGITLKLTTSHF    87
           |  ||| |:|| ::|:.::.|:.: |.|:||::||||
Db      2  LELLSLLSARSGDADVAVAPLIVGLTVESGFEANVAAVVGSRTTGLGGTAVSLKLMPSHY    61

Qy     88  YPSVFVFHGGKHVLPSSAAPNLTRACNAARERFGFSRCQGPPVDGAVETTGAEICTRLGL   147
           :||::||||||.::: :||||  |||:||  |||:||::|||  |||||||
Db     62  SPSVYVFHGGRHLAPSTQAPNLTRLCERARRHFGFSDYAPRPCDLKHETTGDALCERLGL   121

Qy    148  EPENTILYLVVTALFKEAVFMCNVFLHYGGLDIVHINHGDVIRIPLFPVQLFMPDVNRLV   207
           :|: .:||||| |||::: :||||: |: |||||| |:::: |:||||
Db    122  DPDRALLYLVITEGFREAVCISNTFLHLGGMDKVTIGDAEVHRIPVYPLQMFMPDFSRVI   181

Qy    208  PDPNTHRSIGEGFVYPTPFYNTGLCHLIHDCVIAPMAVALRVRNVTAVARGAAHLAFD   267
           |||||||||||||:||||||||||||||||||||||||||||||||:|| ||||||||
Db    182  ADPFNCNHRSIGENFNYPLPFFNRPLARLLFEAVVGPAAVALRARNVDAVARAAAHLAFD   241

Qy    268  ENHEGAVLPPDITVTYFQSSSSGTTTAGAR   298
           |||||| | | |||||:||. :. :|.|.|
Db    242  ENHEGAALPADITFTAFRASQG--KPQRGAR   270


RESULT 7
US-10-237-551-230
;   Sequence 230, Application US/10237551
;   Publication No. US20030165820A1
;   GENERAL INFORMATION:
;   APPLICANT: Day, Craig H.
;   APPLICANT: Hosken, Nancy A.
;   APPLICANT: Parsons, Joseph M.
;   TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
;   TITLE OF INVENTION: TREATMENT OF HERPES SIMPLEX VIRUS INFECTION
;   FILE REFERENCE: 210121.538C3
;   CURRENT APPLICATION NUMBER: US/10/237,551
;   CURRENT FILING DATE: 2002-09-06
;   NUMBER OF SEQ ID NOS: 254
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 230
;   LENGTH: 248
;   TYPE: PRT
;   ORGANISM: Herpes simplex virus
US-10-237-551-230

Query Match          11.7%;    Score 736;   DB 14;   Length 248;
Best Local Similarity 57.7%;    Pred. No. 4e-64;
Matches 139;   Conservative  36;   Mismatches  66;   Indels  0;   Gaps  0;

Qy     47  PLMRNLTVEKTFTSSLAVVSGARTTGLAGAGITLKLTTSHFYPSVFVFHGGKHVLPSSAA   106
           |||.|  ||| ||:|:|.:||||||||.|:||| :|:. |||||:|||||.||| |.
Db      3  PLIVGLTVESGFEANVAAVVGSRTTGLGGTAVSLKLMPSHYSPSVYVFHGGRHLAPSTQA    62

Qy    107  PNLTRACNAARERFGFSRCQGPPVDGAVETTGAEICTRLGLEPENTILYLVVTALFKEAV   166
           |||||  ||||||||||| || ||||| ||||| || |||:||:|:||| |:||.||||
Db     63  PNLTRLCERARRHFGFSDYAPRPCDLKHETTGDALCERLGLDPDRALLYLVITEGFREAV   122

Qy    167  FMCNVFLHYGGLDIVHINHGDVIRIPLFPVQLFMPDVNRLVPDPNTHRSIGEGFVYPT   226
           :||||: |: |||||| |:::. |:||| |: |||| : . |||:|:||||||:|:||
Db    123  CISNTFLHLGGMDKVTIGDAEVHRIPVYPLQMFMPDFSRVIADPFNCNHRSIGENFNYPL   182

Qy    227  PFYNTGLCHLIHDCVIAPMAVALRVRNVTAVARGAAHLAFDENHEGAVLPPDITVTYFQS   286
           |:|||||||||||||||||||||||||:|| ||| |||||||||||| | | ||||:||.
Db    183  PFFNRPLARLLFEAVVGPAAVALRARNVDAVARAAAHLAFDENHEGAALPADITFTAFEA   242

Qy    287  S   287
```

```
Db         243  S  243

RESULT 8
US-10-156-761-9121
;   Sequence 9121, Application US/10156761
;   Publication No. US20030119018A1
;   GENERAL INFORMATION:
;   APPLICANT: OMURA, SATOSHI
;   APPLICANT: IKEDA, HARUO
;   APPLICANT: ISHIKAWA, JUN
;   APPLICANT: HORIKAWA, HIROSHI
;   APPLICANT: SHIBA, TADAYOSHI
;   APPLICANT: SAKAKI, YOSHIYUKI
;   APPLICANT: HATTORI, MASAHIRA
;   TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
;   FILE REFERENCE: 249-262
;   CURRENT APPLICATION NUMBER: US/10/156,761
;   CURRENT FILING DATE: 2002-05-29
;   PRIOR APPLICATION NUMBER: JP 2001-204089
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-272697
;   PRIOR FILING DATE: 2001-08-02
;   NUMBER OF SEQ ID NOS: 15109
;   SEQ ID NO 9121
;   LENGTH: 850
;   TYPE: PRT
;   ORGANISM: Streptomyces avermitilis
US-10-156-761-9121

Query Match           2.0%;    Score 123.5;   DB 14;   Length 850;
Best Local Similarity 20.5%;    Pred. No. 0.046;
Matches 182;   Conservative 104;   Mismatches 327;   Indels 273;   Gaps  37;

Qy    305  TSKPSPSGGFE-------RRLASIMAADTALHAEVIFNTGIYEETPTDIKEWPMFIGM   355
           || |||.||||       | :||        |:|  .:|. :||            | |
Db      3  TSRRTPSGAEPPSRPVRGRRAHAGQPADE-------DTGTDETVTAASADSPVGAGR    54

Qy    356  EGTLPR-------------------LNALGSYTARVAGVIGAMVFSPNSALYLTEVEDSGMTE   399
           | .|                     :: :|
Db     55  WGVRPRTVRAKIVCLLMVPVSLLALWAY-------ATVSTAQDVARLRQVQQVDTTV   105

Qy    400  AKDGGPGPSFNRPYQFAGPHLAANPQTDRDGHVLSSQSTGSSNTEFSVDYLAL----ICG   455
           |  ||  |:|          |         || ::|| : :|.:||: :||
Db    106  RAPVAAAVAALQABRAAAVRHVIDPSAEPD---SGFRTLAARTDRAVDKLRIGGHHTVA   161

Qy    456  FGAPLLARLLFYLERCDAGAFTGGHGDALKYVTGTFDSEIPCSLCEKHTRPVCAHTTVHR   515
           | ||| | :|| :  |               ||  | | :          :| .   |:
Db    162  DGADLPAQVPGRLETFVSGA-------EQLRSLRG----------------AVLER   194

Qy    516  LRQRMPRFGQATRQPIGVFGTMN--SQYSDCDFLGNYAPYLIIRKPGDQTEAAKATMQDT   573
           | |  |            |      :|:                 |  ||  :|  .|.|
Db    195  RARWDETFGQYRTIAAAFGVGGALTGIQDAD-LGSDARVLL-----EFSRAGEALAQED   248

Qy    574  YRATLERLFIDLEQERL-LDRGAPCSSEGLS-SVIVDHPTFRRILDTLRARIEQTTTQFM   631
           ||  ||            |||             |                  |:  .  |
Db    249  AVLSSARLAGTLDGERLRLFTGAVDTRRTLTDSAVAD------LSERERAAWQGVATGRA   302

Qy    632  KVLVETRDYKI---REGLSEATHSMALTFDP-------------------YSGAFCPITN   669
           |:          :|       |:|| |
Db    303  YADVRTAEDKVLANRPGARRIAAAPQATWDPAHARVQEGMRTIEADAGRGVADRADPLTR   362

Qy    670  FLVXRTHLAVVQDIALSQCHCVF------YGQQVEGRNFRNQFQPVLRRRFVD---LFNG   720
           |     |  . .                  :|  |:                 :| |:|
Db    363  GLLTPAGAVLFGLAAVAASLVISVRIGRGLVIELISLRNSALEIARRKLPQAWRKLRAG   422

Qy    721  GFISTRSITVTLSEGPVSAP-NPTLGQDAPAGRTFDGDLARVSVEVIRDIRVKNRVVFSG   779
           |            .| |      ||
Db    423  EEIDVR------AEAPPGPPAEBDETGQVAEALSTVHRAALRAAVE------    461

Qy    780  NCTNLSEARARLVGLASAYQRQEKRVDMLHGALGFLLKQFHGILLFPRGMPENSKSPNPQ   839
           .                              ||
Db    462  ---------------------------RAELASGISGV--------    472
```

```
Db   502 DPSPHLEWLLADGSKVRAPYVSEDGRILIDKNGKLELQMADSFDAGLYHCISTNDADADV 561
                                                           :|
Qy   640 --YKIR--EGLSEATHSMALTFDPYSGAF----CPITNFLVKRTHLAVVQDLALSQCHCV 691
            :||                       :||            : :||
Db   562 LTYRITVVEPYGESTHDSGVQHTVVTGETLDLPCLSTG----------VPDASIS--WI 608
Qy   692 FYGCQVEGRNFRNQFQPVLRRRFVDLFNGGFISTRSITVTLSEGPVS--APNPT------ 743
                                       :|:|:          |
Db   609 LPGNTVFSQPSRDR----------QILNGTLRILQVT-PKDQGHYQCVAANPSGADFSS 657
Qy   744 -------LGQDAFAGRTFDGDLARVSVEVIRDIRVKNRVVFSGNCTNLSEAARAR 791
                                         :  ::||
Db   658 FKVSVQKKGQRMVEHDREAGGSGLGE-PNSSVSLKQPASLK----LSASALTGSEAGKQ- 711
Qy   792 LVGLASAYQREKRVDMLHGALG-FLLKQFHGLLFPRGMPPNSKSPNPQWFWTLLQ---R 847
                                    :||
Db   712 ----VSGVHRKNKHRDLIHRRRGDSTLRRFRE--HRRQLPLSARRIDPQRWAALLEKAKK 765
Qy   848 NQMPADKLTHEEITT------IAAVKRFTEEYAAINFINLPPTCIGELAQFYMANLILK 900
             |                          ||
Db   766 NSVP----KKQENTTVKPVPLAVPLVELTDEEKDASGMI--PP--------------- 802
Qy   901 YCDHSQYLINTLTSIITGARRPRDPSSVLHWIRKDVTSAADIETQAKALLEKTENLPELW 960
             :|:                               :  :  :  :|
Db   803 --DEEFMVLKTKASGVPGRSPTADSGPVNHGFMTSIASGTEVSTVNPQTLQ-SEHLPDFK 859
Qy   961 TTAFTSTHLVRAAM----------NQRPMVVLGISISKYHGAAGNNRVFQAGNWSG-- 1006
Db   860 LFSVNGTAVTKSMNPSIASKIEDTTNQNPIIIFP-SVAEIRDSA------QAGRASSQS 912
Qy  1007 ---LNGGKNVCPLFTFDRTRRFIIACPRGGFI----------------CPVTG--PSSGN 1045
              :||
Db   913 AHPVTGGN---MATYGHINTYSSFTSKASTVLQPINPTESYGPQIPITGVSRPSSSD 966


RESULT 10
US-10-206-576-358
; Sequence 358, Application US/10206576
; Publication No. US20030017495A1
; GENERAL INFORMATION:
;   APPLICANT: Choi et al.
;   TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
;   NUMBER OF SEQUENCES: 497
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Human Genome Sciences, Inc.
;     STREET: 9410 Key West Avenue
;     CITY: Rockville
;     STATE: Maryland
;     COUNTRY: USA
;     ZIP: 20850
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: CD-R
;     COMPUTER: Dell Latitude
;     OPERATING SYSTEM: Windows 98
;     SOFTWARE: ASCII Text
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/10/206,576
;     FILING DATE: 29-Jul-2002
;     CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 09/071,035
;     FILING DATE: 1998-05-04
;     APPLICATION NUMBER: US 60/046,655
;     FILING DATE: 1997-05-16
;     APPLICATION NUMBER: US 60/044,031
;     FILING DATE: 1997-05-06
;     APPLICATION NUMBER: US 60/066,009
;     FILING DATE: 1997-11-14
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Hyman, Mark J.
;     REGISTRATION NUMBER: 46,789
;     REFERENCE/DOCKET NUMBER: PB369P1D1
; INFORMATION FOR SEQ ID NO: 358:
```

```
Qy   840 WFWTLLQRNQMPADKLTHEEITTIAAVKRFTEEYAAINFINLPPTCIGELAQFYMANLIL 899
                         ::|::|:|::           :  :|:
Db   473 -FVNLARRSQI----LVHRQLSLLDSMERRSED----------PNELSDL--FRLDHLTT 515
Qy   900 KYCDHSQYLINTLTSIITGA--RRPRDPSSVLHWIRKDVTSAAD------IETQ----- 945
             :|:                    :|:                    ||
Db   516 RMRRHAESLI----ILSGAAPGRAWRMPVSLTNVVRAAVSEVEDYARVEVRQLPEASVV 570
Qy   946 AKALLEKTENLPELWTTA--FTSTHLVRAAMNQRP------MVVLGISISKYHGAAGN 995
              :|:  : :|::         :|:  :||
Db   571 GAAVADLTHLMAEIVENAAQFSPPH-TRVRVTGEPVGNGYAVEVEDRGLGMGKETLAEAN 629
Qy   996 NRVFQAGNWSGLNGGKNVCPLFTFDRTRRFIIA------------CPRGGFICPVTGP 1041
             :|                      :                    |
Db   630 RRIEQS--------EALDLFDSDRLGLFVVSRLAARHGIKVHLRTSPYGGTTAVVLLP 679
Qy  1042 S---SGNRETT--LSDQVRGIIVSGGAMVQLAIYATVVRAVGARA 1081
            :         :|                  :||||
Db   680 TALLHSGTAERVPRAADTGRD-AEPAYARVAAASHQSVQQAVGRPA 724


RESULT 9
US-10-454-351-34
; Sequence 34, Application US/10454351
; Publication No. US20040053301A1
; GENERAL INFORMATION:
;   APPLICANT: Quark Biotech Inc.; Paz Binat, et al
;   TITLE OF INVENTION: GENES ASSOCIATED WITH MECHANICAL STRESS, EXPRESSION PRODUCTS THERE
;   TITLE OF INVENTION: AND USES THEREOF
;   FILE REFERENCE: 010/PCT2-US2; EINAT=7E
;   CURRENT APPLICATION NUMBER: US/10/454,351
;   CURRENT FILING DATE: 2003-06-04
;   PRIOR APPLICATION NUMBER: US 09/991,630
;   PRIOR FILING DATE: 2001-11-06
;   PRIOR APPLICATION NUMBER: US 09/905,129
;   PRIOR FILING DATE: 2001-07-13
;   PRIOR APPLICATION NUMBER: US 09/802,318
;   PRIOR FILING DATE: 2001-03-08
;   PRIOR APPLICATION NUMBER: US 09/729,485
;   PRIOR FILING DATE: 2000-12-04
;   PRIOR APPLICATION NUMBER: US 09/312,216
;   PRIOR FILING DATE: 1999-05-14
;   NUMBER OF SEQ ID NOS: 37
;   SOFTWARE: PatentIn version 3.0
; SEQ ID NO 34
;   LENGTH: 2597
;   TYPE: PRT
;   ORGANISM: Rattus rattus
US-10-454-351-34

Query Match          2.0%;   Score 123.5;   DB 12;   Length 2597;
Best Local Similarity  18.6%;   Pred. No. 0.33;
Matches  145;  Conservative 114;  Mismatches 286;  Indels 233;  Gaps  40;


Qy   416 AGPHLAANPQTD--RDGHVLSSQSTGSSN-------------------TEFSVDYLALICG 455
             :|                                          :  :|
Db   274 SGAFLCTKPTIDPSLKSKSLVTQEDNGSASTSPQDFIEPFGSLSLNMTDLSGNKADMVCS 333
Qy   456 FGAPLLARLLFYLERCDAGAFTGGHGDALKYVTGTFDSEIPCSLCEKHTRPV----CAHT 511
             ||                    :: |:      ||:           :||
Db   334 IQKP--------SRTSPTAFTEENDYIM--LNASFSTNLVCSVDYNHIQPWQLIALYS 382
Qy   512 TVHRLRQRMP--------RFGQATRQPIGVFGTMNSQYSDCDPLGNYAPYLILRKPGD 561
             :|                  :|                  ::||
Db   383 DSPLILERKPQLTETPSLSSRYKQVALRPEDIFTSIRADVR-ADPFWFQQEKIVLQLNRT 441
Qy   562 QTEAAKATMQDTYRATLERLFIDLEQERL---------LDR------GAPCSSEG 601
             :||                   :|:         :|       :||
Db   442 ATTLSTLQIQFSTDAQIALPRAEMRAERLKWTMILMMNPKLERTVLVGGTIALSCPGKG 501
Qy   602 -----LSSVIVDHPTFR-------RILDTLRARIE-QTTTQFMKVL---VETRD----- 639
                 :|                  :||
```

```
          SEQUENCE CHARACTERISTICS:
              LENGTH: 1074 amino acids
              TYPE: amino acid
              STRANDEDNESS: single
              TOPOLOGY: linear
          MOLECULE TYPE: protein
          SEQUENCE DESCRIPTION: SEQ ID NO: 358:
  US-10-206-576-358:

  Query Match          2.0%;  Score 123; DB 12; Length 1074;
  Best Local Similarity  18.3%; Pred. No. 0.078;
  Matches 206;  Conservative 150; Mismatches 415; Indels 352; Gaps 52;

  Qy   250 RVRNVTAVARGAAHLAFDENHEGAVLPPDITYTYFQSSSSGTTARGARRNDVNSTSKPS 309
                  :::::   ::        :::     :::::  ::::
  Db    67 RTTSLYABYNGAKQTVFC-IEPGVSIPTEVTHGY--------------QKNPL 104

  Qy   310 PSGGFERRLASIM--AADTALHAEVIFNTGIYEB----------------TPTDIKEWPMFI 353
                  :::::       ::   :  :      ::
  Db   105 PSMSDKAKLVSVLWEKAGTDIDTNMVAQKMIWEEVNGYKLHSIKRLGGASVDIK------ 158

  Qy   354 GMEGTLPRLNALGSYTAR------VAGVIG-AMVFSFNSALYLTEVEDSGMTEAKDGGP 405
                  ::::               :: ::
  Db   159 SIEGKINK-AIEBYQKKPSFHNTTVKTIILGQSTLIDKNELNiSEPDKVVQNTA----- 211

  Qy   406 GPSFNRFYQPAGPHLAANPQTDRDGHVLSSQSTGSSNTEFSVDYLALICGFGAPLLARLL 465
                  ::  :              ::::
  Db   212 ---NIDYRVIGNQLVLTP--------------NSNSKSGTLTLKKSAGTGTP-VAYKK 251

  Qy   466 FYLERCDAGAFTGGHGDALKYVTGTFDSEIPCSLCEKHTRPVCAHTTVHRLRQRMPRFGQ 525
                  :::                               ::::
  Db   252 AGLQTVMAGALDKPNTYAIKINVETKGS-LKIKKIDKESGDIVPETVFHL-------DFGK 304

  Qy   526 A------TRQPIGVFGTMNSQYSDCDPLGNYA----------PYLILRKPGDQTEAAKATM 570
           :                                         :::::
  Db   305 ALPSKDVTTDKDGI------SILDGIPHGTKVTITEKSVPDPYMIDTTPMAATIKAGETI 358

  Qy   571 QDTYRATLERLFIDLEQERLLDRGAPCSSEGLS------SVIVDHPT--FRRILDTLRA 621
                  :::::                            :   :::::
  Db   359 SMTSKNMRQKGQILLEKTG-VETGTDLWNDNYSLAGNTFAIRKDSPAGEIVQEITTDEKG 417

  Qy   622 RIEQTTTQFMKVLVETRDYKIREGLSEATHSMALTFDP------YSGAFCPIITNPLVKRT 675
                  :::                               ::::
  Db   418 RAE--TPKELANALELGTYVVTE--TKSSNGFVNTFKPTKVELKYANQTVALVTSNVKGQ 473

  Qy   676 HLAVVQDLAL---------SQCHCVFYGGQV-----EGRNFRNQFQPVLRRRFVDL 717
                  :::                            :::::
  Db   474 NQBITGETTLTKEDKDTGNESQGKAEFKGAEYTLFTAKDGQAVKWSEAFK------TEL 526

  Qy   718 FNGGFISTRSITVTLSB-GPVSAPNPTLGQ------DAPAGRTFDGDLARVSVB------ 764
                  :::                            :::
  Db   527 VKGTKASDETVTLALDBKNQVAVKHLAINEYFWQETKAPEGYTLDETKYPVSIKKVDNNE 586

  Qy   765 ---VIRDIRVKNRVV---------FSGNCTNLSEAA------RARLVGLASAYQRQBKR 805
                  :: :                       :::  :
  Db   587 KNAVITRDVTAKEQVIRFGFDFFKFAGSADGTAETGFNDLSFKVSPLEGTXEITGAEDKA 646

  Qy   806 VDMLHGALGF--------LLKQFHGLLFPRGM----PPNSKS------PNP 838
                  :::            :::
  Db   647 TTACNEQLGFDGYGKFENLPYGDYLLEBIEA---PEGFQKITPLEIRSTFKENKDDYAKS 703

  Qy   839 QWFWTLLQRNQ---------MPADKLTHEBITTIAAVKRFTEYAAINPINLP--PTCIGE 888
                  :: :                        ::
  Db   704 EYVFFITEEGQKQPIKMVTVPYEKLTNNE--------FSVSLNRLMLYDLPEKEDSLTS 754

  Qy   889 LAQFYMANLLIKYCDHSQYLINTLTSIITGARRPRDPSSVLHWIRKD---VTSAADIETQ 945
                  :::                             ::: :::
  Db   755 LATWKDGNKKLNTLDFTE-LVDKL------------RYNLHEIKEDWYYVAQAIDVEA- 799

  Qy   946 AKALLEKTENLPELWTTAFTST----------HLVRAAMNQRPMVLGISISKYHGA 992
                  :::                   :::
  Db   800 TKAAQBKDEKAKPVVIAETTATLANKEKTGTWKILHKLTABQ------VLDKSIVLFNTV 853
```

```
  Qy   993 AGNNRVFQAGNWSGLNGGKNVCPLFTFDRTRRFIIACPRGGFICPVTGPSSGNRETTLSD 1052
                  :::                               :: ::::
  Db   854 YENKVAFFAGNE---------------------------PVA------KDASLNN 875

  Qy  1053 QVRGIIVSGGAMVQLAIYATVVRAVGAR------AQHMAFDDWLSLITDDEFLARDI-- 1102
                  :::                               ::::::
  Db   876 QAQ-----------TVNCTIERHVSIQTKAHLEDGSQTFTHGDVMDMFDDVSVTHDVLD 923

  Qy  1103 -BELHDQIIQTLETPWTVEGALEAVKILDE------KTTAGD--GETPTNLAFNFD 1149
                  :: ::                              ::::
  Db   924 GSKEAFETILYALLPDGTNKEIWKSGKIEHEVNDKEFTKTVLAEKVDTGKYPEGTKFTF- 982

  Qy  1150 SCEPSHDTTSNV--------LNISGSNISGSTVPGLKRPPEDDE 1185
                  :::                        ::  :
  Db   983 -TEINYEKDGNVNGKHNEDLKEKSQTLTPKEVTIPSTPKQPE 1024


  RESULT 11
  US-10-206-576-394
  ; Sequence 394, Application US/10206576
  ; Publication No. US2003001749SA1
  ; GENERAL INFORMATION:
  ;    APPLICANT: Choi et al.
  ;    TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
  ;    NUMBER OF SEQUENCES: 497
  ;    CORRESPONDENCE ADDRESS:
  ;       ADDRESSEE: Human Genome Sciences, Inc.
  ;       STREET: 9410 Key West Avenue
  ;       CITY: Rockville
  ;       STATE: Maryland
  ;       COUNTRY: USA
  ;       ZIP: 20850
  ;    COMPUTER READABLE FORM:
  ;       MEDIUM TYPE: CD-R
  ;       COMPUTER: Dell Latitude
  ;       OPERATING SYSTEM: Windows 98
  ;       SOFTWARE: ASCII Text
  ;    CURRENT APPLICATION DATA:
  ;       APPLICATION NUMBER: US/10/206,576
  ;       FILING DATE: 29-Jul-2002
  ;       CLASSIFICATION: <Unknown>
  ;    PRIOR APPLICATION DATA:
  ;       APPLICATION NUMBER: US 09/071,035
  ;       FILING DATE: 1998-05-04
  ;       APPLICATION NUMBER: US 60/046,655
  ;       FILING DATE: 1997-05-16
  ;       APPLICATION NUMBER: US 60/044,031
  ;       FILING DATE: 1997-05-06
  ;       APPLICATION NUMBER: US 60/066,009
  ;       FILING DATE: 1997-11-14
  ;    ATTORNEY/AGENT INFORMATION:
  ;       NAME: Hyman, Mark J.
  ;       REGISTRATION NUMBER: 46,789
  ;       REFERENCE/DOCKET NUMBER: PB369P1D1
  ; INFORMATION FOR SEQ ID NO: 394:
  ;    SEQUENCE CHARACTERISTICS:
  ;       LENGTH: 1074 amino acids
  ;       TYPE: amino acid
  ;       STRANDEDNESS: single
  ;       TOPOLOGY: linear
  ;    MOLECULE TYPE: protein
  ;    SEQUENCE DESCRIPTION: SEQ ID NO: 394:
  US-10-206-576-394:

  Query Match          2.0%;  Score 123; DB 12; Length 1074;
  Best Local Similarity  18.3%; Pred. No. 0.078;  Gaps 52;
  Matches 206;  Conservative 150; Mismatches 415; Indels 352;

  Qy   250 RVRNVTAVARGAAHLAFDENHEGAVLPPDITYTYFQSSSSGTTARGARRNDVNSTSKPS 309
                  :::::   ::        :::     :::::  ::::
  Db    67 RTTSLYABYNGAKQTVFC-IEPGVSIPTEVTHGY--------------QKNPL 104

  Qy   310 PSGGFERRLASIM--AADTALHAEVIFNTGIYEB-------------TPTDIKEWPMFI 353
```

US-10-282-122A-45763

; Sequence 45763, Application US/10282122A
; Publication No. US2004029129A1
; GENERAL INFORMATION:
;   APPLICANT: Wang, Liangsu
;   APPLICANT: Zamudio, Carlos
;   APPLICANT: Malone, Cheryl
;   APPLICANT: Haselbeck, Robert
;   APPLICANT: Ohlsen, Kari
;   APPLICANT: Zyskind, Judith
;   APPLICANT: Wall, Daniel
;   APPLICANT: Trawick, John
;   APPLICANT: Carr, Grant
;   APPLICANT: Yamamoto, Robert
;   APPLICANT: Forsyth, R.
;   APPLICANT: Xu, H.
;   TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
;   FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
;
; SEQ ID NO 45763
; LENGTH: 2358
; TYPE: PRT
; ORGANISM: Bacillus anthracis
US-10-282-122A-45763

Query Match   1.9%; Score 121; DB 12; Length 2358;
Best Local Similarity 18.7%; Pred. No. 0.5;
Matches 266; Conservative 178; Mismatches 517; Indels 464; Gaps 65;

Qy   57 TFTSSLAVVSGARTTGLAGAGITLKLTTSHFYPSVFVHGGKHVLPSSAAPNLTRACNAA 116
               :: .:|: :|.| :|.: .: :|| :: |
Db   520 TFVANSVIVNGVARPG-ANPASSINLGSINASQTTVV---RFQVRVTSNPLVNPIPNRA 574

Qy   117 RERFGFSRCQG-PPVDG-----AVETT--GAEICTRIGLEP--------ENTI 153
           | :| .:|: | | :.   : :| : | |
Db   575 SATFTFTPVPGQQPVSGQATSNTVVTTINIADIRTRKIVDRAPATVNDVLTYTVIENTG 634

Qy   154 LYLVVTALFKEAVFMCNVFLHYGGLDIVHINEGDVIRIPLFPVQLFMPDVNRLVPDPFNT 213
              : .: . ::|:| .:   :
Db   635 NVLATNVVFQDPIPIGTFI-TNSVTVDGVSQPGANPATGFTVANISPGGSRTV--TFQV 691

Qy   214 HHRSIGEGFVYPTPFYNTGLCHLIHDCVIAPMAVALRVRN-----VTAVARGAAHLAFDE 268
           :   : : : |: .: |. : | . : | :| . | : :
Db   692 RVTSTPSGGTIP----NRG--NVTANFVVIPNQPPITINRQTNTVVTQVNTGGLNVIKEV 745

Qy   269 NHEGAVLPPDITYT------------------YFQSSSS------GTTTARGARRNDVNSTSK 307
              | . | | :   :| ::   .
Db   746 NTTQAVVGDTLTYTTIAVQNTGNVPLTNVFFQDAISSAVSFVANSVTINGVPQSGLN---- 801

RESULT 12

Db   1749 FQATVTNI--------PASGTIINVANITG--SCTLVPG--EPP 1780
             ||:   :|:||:|||::   :|:|||| |||
             (alignment)

RESULT 13
US-09-905-129-2
; Sequence 2, Application US/09905129
; Patent No. US20020137705A1
; GENERAL INFORMATION:
; APPLICANT: Einat, et al
; TITLE OF INVENTION: GENES ASSOCIATED WITH MECHANICAL STRESS, EXPRESSION PRODUCTS THERE
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 540579-2007.2
; CURRENT APPLICATION NUMBER: US/09/905,129
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/802,318
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/207,821
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: 60/084,944
; PRIOR FILING DATE: 1998-05-11
; PRIOR APPLICATION NUMBER: 60/085,673
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.0
;
; SEQ ID NO 2
; LENGTH: 2597
; TYPE: PRT
; ORGANISM: rattus species
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(2597)
; OTHER INFORMATION: 'x' can be any amino acid
US-09-905-129-2

Query Match   1.9%; Score 120.5; DB 9; Length 2597;
Best Local Similarity 18.6%; Pred. No. 0.67;
Matches 145; Conservative 113; Mismatches 287; Indels 233; Gaps 40;

Qy   416 AGPHLAANPQTD---RDGHVLSSQSTGSSNTE--------------FSVDYLALICG 455
               :||:   :: :|:::|||: |:||
Db   274 SGAFLCTKPTIDPSLKSKSLVTQEDNGSASTSPQDFIEPFGSLSLNMTXXSGNKADMVCS 333

Qy   456 FGAPLLARLLFYLERCDAGAFTGGHGDALKYVTGFDSEIPCSLCEKHTRPV----CAHT 511
               ::||||:::::|::   :|:::|::| ::::|
Db   334 IQKP--------SRTSPTAFTEENDYIM--LNASFSTNLVCSVDYNHIQPVWQLLALYS 382

Qy   512 TVIHRLRQRMP--------------RFGGATRQPIGVFGTMNSQYSDCDPLGNYAPYLLLRKPGD 561
               :|:|:|::| ||: | |: :| |:: :| ||: ||:|:|:|||
Db   383 DSPILERKPQLTETPSLLSSRYKQVALRPEDIFTSIEADVR-ADPFWFQQEKIVQLQLNRT 441

Qy   562 QTEAAKATMQDTYRATLERLFIDLEQERL---------------------LDR------GAPCSSEG 601
               |::|:|::|:| :::|:|:||:   :   :|
Db   442 ATTLSTLQFSTDAQIALPRAEMRAERLKWTMILMVMNNPKLERTVLVGGTIALSCPGKG 501

Qy   602 ------LSSVIVDHPTFR------------RILDTLRARIE-QTTTQMKVL----VEIRD------ 639
                     |::::|:| |:|::|::: :::|::|:|
Db   502 DPSPHLEWLLADGSKVRAPYVSEDGRILIDKNGKLELQMADSFPDAGLYHCISTNDADADV 561

Qy   640 --YKIR--EGLSEATHSMALTFDPYSGAF----CPITNFLVKRTHLAVVQDLALSQCHCV 691
                  :::: :|:|: |:|: :|| ||: |::::|:|:|:|:||:|:|::|
Db   562 LTYRITTVEPYGESTHDSGVQHTVVTGETLDLPCLSTG----VPDASIS----WI 608

Qy   692 FYGQQVEGRNFRNQFQPVLRRRFVDLFNGGFISTRSITVTLSEGPVS--APNPT------ 743
               |:|: :||::|:||||::||||::||:|::|::::| :||::|:||:   :|||:
Db   609 LPGNTVFSQPSRDR--------QILNNGTLRILQVT-PKDQHYQCVAANPSGADFSS 657

Qy   744 --------LGQDAPAGRTPDGDLARVSVEVIRDIRVKNRVFSGNCTNLSEAARAR 791
                       ||: | |:|||:|||:|:||:::|:::|::|:|::| |::::|::
Db   658 FKVSVQKKGQRMVEHDREFAGGSGLGE-PNSSVSLKQPASLK----LSASALTGSEAGKQ- 711

Qy   792 LVGLASAYQRQEKRVDMLHGALG-FLLKQFHGLLFPRGMPPNSKSPNPQWFWTLLQ---R 847
               |:|||:|::|:|::||:|:|||| ||::||:|:|: ||:||||||::||:|||:::
Db   (continues)

(left column blocks, top of page, alignment segments:)

Qy   308 PSPSGGFEERLASIMAADTAL----------HAEVIFN------TGIYEETPTDIKEWPMF 352
               :|:|||::|||::|::|:| ||:|:|| :||:|:|||:||||
Db   802 --PNTGFS--LPNIPAAQTVVVTFDVLIIQDPENEDILNQANVTASFQVNPS--EPPVT 854

Qy   353 IGM--------EGTLPRLNALGSYTARVAGVIGAMVFSPNSALYLTEVEDSGMTEAKD 402
               :|: |:|::|::||:|::|||:||:|::|:|:::|::|::|| ::|
Db   855 INVPSNIVNTVQSGNPFEVVKSVNTDVATVGDVL---------VYTIEIINAGSV---- 900

Qy   403 GGPGPSFNRFYQFAGP--------------HLAANPQTIRDRDGHVLSSQSTGSS---NT 443
               |||||:||::|:||| :|:|||||::||:|||:|||:|:|| ||
Db   901 ----PATNVFFQDSIPQGTLPIENSVFVNGVLQEGADPEL--GFPLNDLPTGASVIVTF 953

Qy   444 EFSVDYLALICGFGAPLLARLLFYLERCDAGAFTGGHGDALKYVTGTF---DSEIPCSLC 500
               |||||||||:|||||||||||||||||||||||:||||||||||||| ||||||||
Db   954 EVLIDEIPL---------GNNVVNSANVTGDFLVNPTEPPITVT 988

Qy   501 EKHTRPVCAHTTVHRLRQRMPRFGQATR----------QPIGVFGTMNSQYSDCDPL 547
               |:||||:||||:|:||:|:|:|:|:|:   :||:||||||::|||:|||
Db   989 EPSNTVM--TVVNSSGLNVIKSVSATEAGVGDTLTYTVRIQNSGTVAATNVSFLDPIPS 1045

Qy   548 GN--YAPYLILR--------KPGDQTEAAKATMQDTYRATLERLFIDLEQERLLDRGA--- 595
               || |:|:|:| |||||:||||||||||||||:||||:||:|:||||:
Db   1046 GTTFVANSVIINGTPQPGLNPTTGFPLANIPVGGMVTVAFQVTITSVPPNRVLPNNANVT 1105

Qy   596 ------PCSSEGLSSVIVDHP-------TFRRILDTLRARIEQTTTQFMKVLVETR--- 638
                     |||||:||:|:|:| :||||:|||||:|:|||:|||:|:|::
Db   1106 ADFQVSPLQPPITIVTISNIVVTRVNVGSLNVMKSVNTLQAGVGDTLT--YTILIQNTGT 1163

Qy   639 ---------DYKIREGLSEATHSMALT-------FDPYSGAFCPITNFLVKRTHLAVVQDIA 684
                        |:|:|:|||:|||:|| ||||||:|||||||||||||:|:|:|||:
Db   1164 VPATNIIFQDPIPSGTAFVANSVTINGVVQQGADPMAG--FPVNPIPVGQTATVTFQ-- 1218

Qy   685 LSQCHCVFYGQQVEGRNFRNQFQ----PVLRRRFVDLFNGGFPISTRSITVTL 732
               |::|:|:||||:||||||||:| ::|::|:|:::|:||::|||:||:||
Db   1219 -----VTVTSIPSGGNIRNQSNITASFLINPANPPI----TTVTNSNFVVIQVNTAQL 1267

Qy   733 SEGPVSAPNPTLGQDAPAGRTF----DGDLARVSVEVIRDIR-----VKNRVFSG 779
               |||||:|:||||||||:||:| ||::||:|::|:::| :|:|:|:|
Db   1268 NIQKTSSV------QQAALGETYTYSVVIRNNGTVATNVSFIDPIAPETTFVANSVTING 1322

Qy   780 ---------------------NCTNLSEAARARLVGLASAYQ------------- 800
                                    ||:|||::|:|||:|::|:|
Db   (continues)

Qy   1323 TPQPGFDPNVGFPLPNIAAGTSLTVTFQVTVIAPSTRGAVLNTASAIATFLLNPLQPPVT 1382
               ||:||:|||:|||:|::||:||:||||||:|:|::|||:|::|::|:|:|:||:|||||
Db   801 RQEKRVDMLHGALGFLLKQPHGLLPPRGMPPNSKSPNPQW 840

Qy   1383 TTNSSNTTVTIPLPPPGEVTATKTVDVAAGAVGDVL-TVTVLISNVGIIPVA------- 1434
               |||||:||||:|:|||:|:|:::|:|:|:|:||::| ||||::||||::|
Db   841 FWTLLQRNQMPADKLTHEEITTIAAVKRFTEEYAAINFINLPPTCIGELAQFYMANLILK 900

Qy   1435 --DVFFQDVIPEGTIPVEGSVTIGGVQQLGLN-PEIGFTVTPLLIAGGSIBITFQVTIIE 1491
                 |:|:||:||:|::|:|||:||||::|:|:| :|||:|||::||||::|::|||||::
Db   901 YCDHSQYLINTLTSIITGARRPRDPSSV----------LHWIRKDVTSAAD 941

Qy   1492 IPD-NEVILNDADVTFTSQPNPQEPPITETILTNLVVTTINIAFVPPLKLVDKEVATVGE 1550
               :|| |:|::|||:|:|:||||:|||::||:::||:||:|::|:||||::|:|:|:||:|
Db   942 IETQAKALLEKTENLPELWTTAFTSTHLVRAAMNQRPMVVLGISISKYHGAAGNRVFQA 1001

Qy   1551 ILTY-DVLIFNGTVP----------ATNVQYSDVLPSSIAFEPNSVTIDGVLQP----- 1594
               :|| ::|:||:| |||:|:||:|||:::||:|||:||||||:|
Db   1002 G------NWSGLNGGKNVCPLFTFDRTRRPIIACPRGGFICP---------------- 1037

Qy   1595 GFNPNNGFPLPDINPGESV-EVTFQVT--VVSVPSNGTIVNTANVTGSFVLVPGEPPV 1649
               ||:||:|||||:|||||:| |:|||:| |||:||:|||:|:|||:|:|::|||:|||
Db   1038 -VTGPSSGNERTTLSDQVRGIIVSGGAMVQLAIYATVVRAVGARAQHMAPDDWLSLTDDE 1096

Qy   1650 QFNVIKQVNRAATLVGDVLYTVQITNT-GT 1695
               :|:|::|::||||:|||||:|||::| ||
Db   1097 FLARDLEELHDQIIQTLE-------TPWTVEGALEAVKIIDEKTAGDGETP------- 1141

Qy   1696 QFIDTISAGASFVPNSVTINGALQ-PNLNPITCGFVGVGDIPVGETVVVT 1748
               :||::||:|||:|:|||:||||:| |:||:|||::|||||:||||:||||
Db   1142 -----TNLAFNFDSCEPSHDTTSNVLNISGSNISGSSTVPGLKRPP 1181

Qy   (continues)

RESULT 14

```
RESULT 14
US-09-905-129-10
; Sequence 10, Application US/09905129
; Patent No. US20020137705A1
; GENERAL INFORMATION:
; APPLICANT: Einat, et al
; TITLE OF INVENTION: GENES ASSOCIATED WITH MECHANICAL STRESS, EXPRESSION PRODUCTS THERE
; TITLE OF INVENTION:  AND USES THEREOF
; FILE REFERENCE: 540579-2007.2
; CURRENT APPLICATION NUMBER: US/09/905,129
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/802,318
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/207,821
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: 60/084,944
; PRIOR FILING DATE: 1998-05-11
; PRIOR APPLICATION NUMBER: 60/085,673
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 2597
; TYPE: PRT
; ORGANISM: Rattus sp.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(2597)
; OTHER INFORMATION: 'x' can be any amino acid
US-09-905-129-10

Query Match             1.9%;  Score  120.5;  DB 9;  Length 2597;
Best Local Similarity   18.6%;  Pred. No. 0.67;
Matches  145;  Conservative  113;  Mismatches  287;  Indels  233;  Gaps  40;

Qy    416 AGPHLAANPQTD---RDGHVLSSQSTGSSNTE-----------------FSVDYLALICG 455
              ::    :   :|           ::  |  :                    |:::
Db    274 SGAFLCTKFTIDPSLKSKSLVTQEDNGSASTSPQDFIEPFGSLSLNMTXXSGNKADMVCS 333

Qy    456 FGAPLLARLLFYLERCDAGAFTGGHGDALKYVTGTPDSEIPCSLCEKHTRPV----CAHT 511
              |        :|                :||                 :  |
Db    334 IQKP---------SRTSPTAFTEENDYIM--LNASFSTNLVCSVDYNHIQPVWQLLALYS 382

Qy    512 TVHRLRQRMP---------RFGQATRQPIGVFGTMNSQYSDCDPLGNYAPYLILRKPGD 561
                  :|                 :                |      ::
Db    383 DSPLILERKPQLTETPSLSSYKQVALRPEDIFTSIEADVR-ADPFWFQQEKIVLQLNRT 441

Qy    562 QTEAAAATMQDTYRATLERLFIDLEQERL-----------LDR-------GAPCSSEG 601
                     |||                              ::
Db    442 ATTLSTLQIQFSTDAQIALPRAEMRAERLKWTMILMNNPKLERTVLVGGTIALSCPGKG 501

Qy    602 -----LSSVIVDHPTFR------RILDTLRARIE-QTTTQFMKVL---VETRD----- 639
                    :|                |||                 :|
Db    502 DPSPHLEWLLADGSKVRAPYVSEDGRILIDKNGKLELQMADSFDAGLYHCISTNDADADV 561

Db    712 ----VSGVHRKNKHRDLIHRRGDSTLRRFRE--HRRQLPLSARRIDPQRWAALLEKAKK 765
               |:|                               |||
Qy    848 NQMPADKLTHEEITT------IAAVKRFTEEYAAINFINLPPTCIGELAQFYMANLILK 900

Db    766 NSVP---KKQENTTVKPVPLAVPLVELTDEEKDASGMI--PP----------------- 802
               :|
Qy    901 YCDHSQYLINTLTSIITGARRPRDPSSVLHWIRKDVTSAADIETQAKALLEKTENLPELW 960

Db    803 --DEEFMVLKTKASGVPGRSPTADSGPVNHGFMTSIASGTEVSTVNPQTIQ-SEHLPDFK 859
              ::   |      ::                :::  :  | | ::|:|  |  :|||||||
Qy    961 TTAFTSTHLVRAAM------------NQRPMVVLGISISKYHGAAGNNRVFQAGNWSG-- 1006

Db    860 LFSVTNGTAVTKSMNPSIASKIEDTTNQNPIIIFP-SVAEIRDSA------QAGRASSQS 912
               :                   :                :|:          ||:|||:|
Qy   1007 ---LNGGKNVCPLFTFDRTRRFIIACPRGGFI---------------CPVTG---PSSGN 1045

Db    913 AHPVTGGN---MATYGHTNTYSSFTSKASTVLQPINPTESYGPQIPITGVSRPSSSD 966
              :|: |||                                        ||||||||:
```

RESULT 15

```
Qy    640 --YKIR--EGLSRATHSMALTFPDYSGAF-----CPITNFLVKRTHLAVVQDLALSQCHCV 691
              |:|:                              :|:                :
Db    562 LTYRITVVPEYGESTHDSGVQHTVVTGETLDLPCLSTG---------VPDASIS---WI 608

Qy    692 FYGQQVEGRNFRNQFQPVLRRRFVDLFNGGFISTRSITVTLSEGPVS-APNPT------ 743
                                              :|                 :|||:
Db    609 LPGNTVFSQPSRDR----------QILNNGTLRILQVT-PKDQGHYQCVAANPSGADFSS 657

Qy    744 ---------LGQDAPAGRTFDGDLARVSVEVIRDIRVKNRVVFSGNCTNLSEAARAR 791
                       |:                 ::|
Db    658 FKVSVQKKGQRMVEHDREAGGSGLGE-PNSSVSLKQPASLK----LSASALTGSEAGKQ- 711

Qy    792 LVGLASAYORQEKRVDMLHGALG-FLLKQFHGLLFPRGMPPNSKSPNQWFWTLLQ---R 847
              |:|                                                 |||
Db    712 ----VSGVHRKNKHRDLIHRRGDSTLRRFRE--HRRQLPLSARRIDPQRWAALLEKAKK 765

Qy    848 NQMPADKLTHEEITT------IAAVKRFTEEYAAINFINLPPTCIGELAQFYMANLILK 900
              :|                               |||
Db    766 NSVP---KKQENTTVKPVPLAVPLVELTDEEKDASGMI--PP----------------- 802

Qy    901 YCDHSQYLINTLTSIITGARRPRDPSSVLHWIRKDVTSAADIETQAKALLEKTENLPELW 960
              :|
Db    803 --DEEFMVLKTKASGVPGRSPTADSGPVNHGFMTSIASGTEVSTVNPQTIQ-SEHLPDFK 859

Qy    961 TTAFTSTHLVRAAM------------NQRPMVVLGISISKYHGAAGNNRVFQAGNWSG-- 1006
              ::   |      ::                :::  :  | | ::|:|  |  :|||||||
Db    860 LFSVTNGTAVTKSMNPSIASKIEDTTNQNPIIIFP-SVAEIRDSA------QAGRASSQS 912

Qy   1007 ---LNGGKNVCPLFTFDRTRRFIIACPRGGFI---------------CPVTG---PSSGN 1045
               :                   :                :|:          ||:|||:|
Db    913 AHPVTGGN---MATYGHTNTYSSFTSKASTVLQPINPTESYGPQIPITGVSRPSSSD 966
              :|: |||                                        ||||||||:

RESULT 15
US-09-905-129-13
; Sequence 13, Application US/09905129
; Patent No. US20020137705A1
; GENERAL INFORMATION:
; APPLICANT: Einat, et al
; TITLE OF INVENTION: GENES ASSOCIATED WITH MECHANICAL STRESS, EXPRESSION PRODUCTS THEREI
; TITLE OF INVENTION:  AND USES THEREOF
; FILE REFERENCE: 540579-2007.2
; CURRENT APPLICATION NUMBER: US/09/905,129
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/802,318
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/207,821
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: 60/084,944
; PRIOR FILING DATE: 1998-05-11
; PRIOR APPLICATION NUMBER: 60/085,673
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 2597
; TYPE: PRT
; ORGANISM: Rattus sp.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(2597)
; OTHER INFORMATION: 'x' can be any amino acid
US-09-905-129-13

Query Match             1.9%;  Score  120.5;  DB 9;  Length 2597;
Best Local Similarity   18.6%;  Pred. No. 0.67;
Matches  145;  Conservative  113;  Mismatches  287;  Indels  233;  Gaps  40;

Qy    416 AGPHLAANPQTD--RDGHVLSSCSTGSSNTE------------------FSVDYLALICG 455
              ::    :   :|           ::  |  :                    |:::
Db    274 SGAFLCTKFTIDPSLKSKSLVTQEDNGSASTSPQDFIEPFGSLSLNMTXXSGNKADMVCS 333
```

```
Qy  456 FGAPLLARLLFYLERCDAGAFTGGHGDALKYVTGTFDSEIPCSLCEKHTRPV----CAHT 511
            ::|::    |             ::                          ::
Db  334 IQKP--------SRTSPTAFTEENDYIM--LNASFSTNLVCSVDYNHIQPVWQLLALYS 382

Qy  512 TVHRLRQRMP---------RFGQATRQPIGVFGTMNSQYSDCDPLGNYAPYLILRKPGD 561
             :|:                                      |:
Db  383 DSPLILERKPQLTETPSLSSRYKQVALRPEDIFTSIEADVR-ADPFWFQQEKIVLQLNRT 441

Qy  562 QTEAAKATMQDTYRATLERLFIDLEQERL------LDR------GAPCSSEG 601
                                         |:|        :|
Db  442 ATTLSTLQIQFSTDAQIALPRAEMRAERLKWTMILMNNPKLERTVLVGGTIALSCPGKG 501

Qy  602 ----LSSVIVDHPTFR--------RILDTLRARIE-QTTTQFMKVL----VETRD------ 639
             :||                   |::                     |||
Db  502 DPSPHLEWLLADGSKVRAPYVSEDGRILIDKNGKLELQMADSFDAGLYHCISTNDADADV 561

Qy  640 --YKIR--EGLSEATHSMALTFDPYSGAF----CPITNFLVKRTHLAVVQDLALSQCHCV 691
            |:||     ||::|                         ::
Db  562 LTYRITVVEPYGESTHDSGVQHTVVTGETLDLPCLSTG---------VPDASIS---WI 608

Qy  692 FYGQQVEGRNFRNQFQPVLRRRFVDLFNGGPISTRSITVTLSEGPVS--APNPT------ 743
             ::                                            :|:|
Db  609 LPGNTVFSQPSRDR---------QILNNGTLRILQVT-PKDQGHYQCVAANPSGADFSS 657

Qy  744 ------LGQDAPAGRTFDGDLARVSVEVIRDIRVKNRVVFSGNCTNLSEAARAR 791
             :|                :|    :|               ||:|
Db  658 FKVSVQKKGQRMVEHDREAGGSGLGE-PNSSVSLKQPASLK----LSASALTGSEAGKQ- 711

Qy  792 LVGLASAYQRQEKRVDMLHGALG-FLLKQFHGLLFPRGMPPNSKSPNPQWFWTLLQ--R 847
             :|:| :|            :::|    |:::           ::
Db  712 ----VSGVHRKNKHRDLIHRRRGDSTLRRFRE--HRRQLPLSARRIDPQRWAALLEKAKK 765

Qy  848 NQMPADKLTHEITT-------IAAVKRFTEEYAAINFINLPPTCIGELAQFYMANLILK 900
            |                 |                     ::::
Db  766 NSVP----KKQENTTVKPVPLAVPLVELTDEKDASGMI--PP 802

Qy  901 YCDHSQYLINTLTSIITGARRPRDPSSVLHWIRKDVTSAADIETQAKALLEKTENLPELW 960
             ::                                      :|:||:|:
Db  803 --DEEFMVLKTKASGVPGRSPTADSGPVNHGFMTSIASGTEVSTVNPQTLQ-SEHLPDFK 859

Qy  961 TTAFTSTHLVRAAM-----------NQRPMVVLGISISKYHGAAGNNRVFQAGNWSG-- 1006
            |:    |                           :|:|
Db  860 LFSVTNGTAVTKSMNPSIASKIEDTTNQNPIIIFP-SVAEIRDSA------QAGRASSQS 912

Qy 1007 ---LNGGKNVCPLFTFDRTRRFIIACPRGGFI------------CPVTG---PSSGN 1045
             ::|                            |||          |||
Db  913 AHPVTGGN----MATYGHTNTYSSFTSKASTVLQPINPTESYGPQIPITGVSRPSSSD 966
```

RESULT 16
US-09-991-630-2
; Sequence 2, Application US/09991630
; Patent No. US20020151514A1
; GENERAL INFORMATION:
; APPLICANT: Einat, et al
; TITLE OF INVENTION: GENES ASSOCIATED WITH MECHANICAL STRESS, EXPRESSION PRODUCTS THERE
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 540579-2007.3
; CURRENT APPLICATION NUMBER: US/09/991,630
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: 09/905,129
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/802,318
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 09/729,485
; PRIOR FILING DATE: 2000-12-04
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 2597
; TYPE: PRT
; ORGANISM: Rattus species
; FEATURE:

; NAME/KEY: misc_feature
; LOCATION: (1)..(2597)
; OTHER INFORMATION: 'x' can be any amino acid
US-09-991-630-2

Query Match   1.9%; Score 120.5; DB 9; Length 2597;
Best Local Similarity 18.6%; Pred. No. 0.67;
Matches 145; Conservative 113; Mismatches 287; Indels 233; Gaps 40;

```
Qy                                                  FSVDYLALICG 455
                                                    ::|::
Db  416 AGPHLAANPQTD--RDGHVLSSQSTGSSNTE------
            ||:::                          |:
Db  274 SGAFLCTKPTIDPSLKSKSLVTQEDNGSASTSPQDFIEPFGSLSLNMTXXSGNKADMVCS 333

Qy  456 FGAPLLARLLFYLERCDAGAFTGGHGDALKYVTGTFDSEIPCSLCEKHTRPV----CAHT 511
            ::|::    |             ::                          ::
Db  334 IQKP--------SRTSPTAFTEENDYIM--LNASFSTNLVCSVDYNHIQPVWQLLALYS 382

Qy  512 TVHRLRQRMP---------RFGQATRQPIGVFGTMNSQYSDCDPLGNYAPYLILRKPGD 561
             :|:                                      |:
Db  383 DSPLILERKPQLTETPSLSSRYKQVALRPEDIFTSIEADVR-ADPFWFQQEKIVLQLNRT 441

Qy  562 QTEAAKATMQDTYRATLERLFIDLEQERL------LDR------GAPCSSEG 601
                                         |:|        :|
Db  442 ATTLSTLQIQFSTDAQIALPRAEMRAERLKWTMILMNNPKLERTVLVGGTIALSCPGKG 501

Qy  602 ----LSSVIVDHPTFR--------RILDTLRARIE-QTTTQFMKVL----VETRD------ 639
             :||                   |::                     |||
Db  502 DPSPHLEWLLADGSKVRAPYVSEDGRILIDKNGKLELQMADSFDAGLYHCISTNDADADV 561

Qy  640 --YKIR--EGLSEATHSMALTFDPYSGAF----CPITNFLVKRTHLAVVQDLALSQCHCV 691
            |:||     ||::|                         ::
Db  562 LTYRITVVEPYGESTHDSGVQHTVVTGETLDLPCLSTG---------VPDASIS---WI 608

Qy  692 FYGQQVEGRNFRNQFQPVLRRRFVDLFNGGPISTRSITVTLSEGPVS--APNPT------ 743
             ::                                            :|:|
Db  609 LPGNTVFSQPSRDR---------QILNNGTLRILQVT-PKDQGHYQCVAANPSGADFSS 657

Qy  744 ------LGQDAPAGRTFDGDLARVSVEVIRDIRVKNRVVFSGNCTNLSEAARAR 791
             :|                :|    :|               ||:|
Db  658 FKVSVQKKGQRMVEHDREAGGSGLGE-PNSSVSLKQPASLK----LSASALTGSEAGKQ- 711

Qy  792 LVGLASAYQRQEKRVDMLHGALG-FLLKQFHGLLFPRGMPPNSKSPNPQWFWTLLQ--R 847
             :|:| :|            :::|    |:::           ::
Db  712 ----VSGVHRKNKHRDLIHRRRGDSTLRRFRE--HRRQLPLSARRIDPQRWAALLEKAKK 765

Qy  848 NQMPADKLTHEITT-------IAAVKRFTEEYAAINFINLPPTCIGELAQFYMANLILK 900
            |                 |                     ::::
Db  766 NSVP----KKQENTTVKPVPLAVPLVELTDEKDASGMI--PP 802

Qy  901 YCDHSQYLINTLTSIITGARRPRDPSSVLHWIRKDVTSAADIETQAKALLEKTENLPELW 960
             ::                                      :|:||:|:
Db  803 --DEEFMVLKTKASGVPGRSPTADSGPVNHGFMTSIASGTEVSTVNPQTLQ-SEHLPDFK 859

Qy  961 TTAFTSTHLVRAAM-----------NQRPMVVLGISISKYHGAAGNNRVFQAGNWSG-- 1006
            |:    |                           :|:|
Db  860 LFSVTNGTAVTKSMNPSIASKIEDTTNQNPIIIFP-SVAEIRDSA------QAGRASSQS 912

Qy 1007 ---LNGGKNVCPLFTFDRTRRFIIACPRGGFI------------CPVTG---PSSGN 1045
             ::|                            |||          |||
Db  913 AHPVTGGN----MATYGHTNTYSSFTSKASTVLQPINPTESYGPQIPITGVSRPSSSD 966
```

RESULT 17
US-09-991-630-10
; Sequence 10, Application US/09991630
; Patent No. US20020151514A1
; GENERAL INFORMATION:
; APPLICANT: Einat, et al
; TITLE OF INVENTION: GENES ASSOCIATED WITH MECHANICAL STRESS, EXPRESSION PRODUCTS THERE
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 540579-2007.3
; CURRENT APPLICATION NUMBER: US/09/991,630
; CURRENT FILING DATE: 2001-11-06

```
RESULT 18
US-09-991-630-13
; Sequence 13, Application US/0991630
; Patent No. US20020151514A1
; GENERAL INFORMATION:
;   APPLICANT: Einat, et al
;   TITLE OF INVENTION: GENES ASSOCIATED WITH MECHANICAL STRESS, EXPRESSION PRODUCTS THEREO
;   TITLE OF INVENTION:  AND USES THEREOF
;   FILE REFERENCE: 540579-2007.3
;   CURRENT APPLICATION NUMBER: US/09/991,630
;   CURRENT FILING DATE:    2001-11-06
;   PRIOR APPLICATION NUMBER: 09/905,129
;   PRIOR FILING DATE: 2001-07-13
;   PRIOR APPLICATION NUMBER: 09/802,318
;   PRIOR FILING DATE: 2001-03-08
;   PRIOR APPLICATION NUMBER: 09/729,485
;   PRIOR FILING DATE: 2000-12-04
;   NUMBER OF SEQ ID NOS: 28
;   SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
;   LENGTH: 2597
;   TYPE: PRT
;   ORGANISM: Rattus species
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(2597)
;   OTHER INFORMATION: 'x' can be any amino acid
US-09-991-630-13

Query Match     1.9%;   Score 120.5;  DB 9;  Length 2597;
Best Local Similarity   18.6%;  Pred. No. 0.67;
Matches 145;  Conservative 113;  Mismatches 287;  Indels 233;  Gaps 40;

Qy   416  AGPHLAANPQTD--RDGHVLSSQSTGSSNTE----------------FSVDYLALICG  455

Db   274  SGAFLCTKPTIDPSLKSKSLVTQEDNGSASTSPQDFIEPFGSLSLNMTXXSGNKADMVCS  333

Qy   456  FGAPLLARLLFYLERCDAGAFTGGHGDALKYVTGTFDSEIPCSLCEKHTRPV----CAHT  511

Db   334  IQKP--------SRTSPTAFTEENDYIM--LNASFSTNLVCSVDYNHIQPVWQLLALYS  382

Qy   512  TVHRLRQRMP---------RFGQATRQPIGVFGTMNSQYSDCDPLGNYAPYLILRKPGD  561

Db   383  DSPLILERKPQLTETPSLSSRYKQVALRPEDIFTSIEADVR-ADPFWFQQEKIVLQLNRT  441

Qy   562  QTEAAKATMQDTYRATLERLFIDLEQERL---------LDR-------GAPCSSEG  601

Db   442  ATTLSTLQIQFSTDAQIALPRAEMRAERLKWTMILMMNNPKLERTVLVGGTIALSCPGKG  501

Qy   602  -----LSSVIVDHPTFR---------RILDTLRARIE-QTTTQFMKVL------VETRD---  639

Db   502  DPSPHLEWLLADGSKVRAPYVSEDGRILIDKNGKLELQMADSFDAGLYHCISTNDADADV  561

Qy   640  --YKIR--EGLSEATHSMALTFDPYSGAF----CPITNFLVKRTHLAVVQDLALSQCHCV  691

Db   562  LTYRITVVEPYGESTHDSGVQHTVVTGETLDLPCLSTG--------VPDASIS--WI  608

Qy   692  FYGQQVEGRNFRNQFQPVLRRRFVDLFNGGFISTRSITVTLSEGPVS-APNPT-------  743

Db   609  LPGNTVFSQPSRDR------------QILNNGTLRILQVT-PKDQGHYQCVAANPSGADFSS  657

Qy   744  ---------LGQDAPAGRTFDGDLARVSVEVIRDIRVKNRVVFSGNCTNLSEAARAR  791

Db   658  FKVSVQKKGQRMVEHDREAGGSGLGE-PNSSVSLKQPASLK----LSASALTGSEAGKQ-  711

Qy   792  LVGLASAYQREKRVDMLHGALG-FLLKQFHGLLFPRGMPPNSKSPNPQWFWTLLQ---R  847

Db   712  ----VSGVHRKNKHRDLIHRRRGDSTLRRFRE--HRRQLPLSARRIDPQRWAALLEKAKK  765

Qy   848  NQMPADKLTHEITT-------IAAVKRFTEYAAINFINLPPTCIGELAQFYMANLILK  900
```

```
Db   562  LTYRITVVEPYGESTHDSGVQHTVVTGETLDLPCLSTG------------VPDASIS---WI  608

Qy   692  FYGQQVEGRNFRNQFQPVLRRRFVDL-FNGGFISTRSIVTLSEGPVS--APNPT-------  743

Db   609  LPGNTVFSQPSRDR------------QIINNGTLRILQVT-PKDQGHYQCVAANPSGADFSK  657

Qy   744  ------------LGQDAPAGRTFDGDLARVSVEVIRDIRVKNRVVFSGNCTNLSEAARAR  791

Db   658  FKVSVQKKGQRMVEHDREAGGSGLGE-PNSSVSLKQPASLK---LSASALTGSEAGKQ-  711

Qy   792  LVGLASAYQRQEKRVDMLHGALG-FLLKQFHGLLFPRGMPPNSKSPNPQWFWTLLQ--R  847

Db   712  --VSGVHRKNKHRDLIHRRRGDSTLRRFRE--HRRQLPLSARRIDPQRWAALLEKAKK  765

Qy   848  NQMPADKLTHEITT------------IAAVKRFTEYAAINFINLPPTCIGELAQFYMANLILK  900

Db   766  NSVP-----KKQENTTVKPVPLAVPLVELTDEEKDASGMI--PP-------------------  802

Qy   901  YCDHSQYLINTLTSIITGARRPRDPSSVLHWIRKDVTSAADIETQAKALLEKTENLPELW  960

Db   803  --DEEFMVLKTKASGVPGRSPTADSGPVNHGFMTSIASGTEVSTVNPQTLQ-SEHLPDFK  859

Qy   961  TTAFTSTHLVRAAM------------NQRPMVVLGISISKYHGAAGNNRVFQAGNWSG--  1006

Db   860  LFSVTNGTAVTKSMNPSIASKIEDTTNQNPIIIFP-SVAEIRDSA------QAGRASSQS  912

Qy   1007 ---LNGGKNVCPLFTFDRTRRFIIACPRGGFI------------CPVTG----PSSGN  1045

Db   913  AHPVTGGN---MATYGHTNTYSSFTSKASTVLQPINPTESYGPQIPITGVSRPSSSD  966
```

RESULT 20
US-10-454-351-10
; Sequence 10, Application US/10454351
; Publication No. US20040053301A1
; GENERAL INFORMATION:
; APPLICANT: Quark Biotech Inc.; Paz Einat, et al
; TITLE OF INVENTION: GENES ASSOCIATED WITH MECHANICAL STRESS, EXPRESSION PRODUCTS THERE
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 010/PCT2-US2; EINAT=7E
; CURRENT APPLICATION NUMBER: US/10/454,351
; CURRENT FILING DATE: 2003-06-04
; PRIOR APPLICATION NUMBER: US 09/991,630
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 09/905,129
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 09/802,318
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 09/729,485
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: US 09/312,216
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.0
;
; SEQ ID NO 10
;   LENGTH: 2597
;   TYPE: PRT
;   ORGANISM: Rattus species
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(2597)
;   OTHER INFORMATION: 'x' can be any amino acid
US-10-454-351-10

```
Query Match        1.9%;     Score 120.5;  DB 12;  Length 2597;
Best Local Similarity  18.6%;  Pred. No. 0.67;
Matches  145;   Conservative  113;  Mismatches  287;  Indels  233;  Gaps  40;

Qy   416  AGPHLAANPQTD--RDGHVLSSQSTGSSNTE------------FSVDYLALICG  455
              :::::||         |:::||              ::|
Db   274  SGAFLCTKPTIDPSLKSKSLVTQEDNGSASTSPQDFIEPFGSLSLNMTXXSGNKADMVCS  333
```

RESULT 19
US-10-454-351-2
; Sequence 2, Application US/10454351
; Publication No. US20040053301A1
; GENERAL INFORMATION:
; APPLICANT: Quark Biotech Inc.; Paz Einat, et al
; TITLE OF INVENTION: GENES ASSOCIATED WITH MECHANICAL STRESS, EXPRESSION PRODUCTS THERE
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 010/PCT2-US2; EINAT=7E
; CURRENT APPLICATION NUMBER: US/10/454,351
; CURRENT FILING DATE: 2003-06-04
; PRIOR APPLICATION NUMBER: US 09/991,630
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 09/905,129
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 09/802,318
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 09/729,485
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: US 09/312,216
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.0
;
; SEQ ID NO 2
;   LENGTH: 2597
;   TYPE: PRT
;   ORGANISM: Rattus species
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(2597)
;   OTHER INFORMATION: 'x' can be any amino acid
US-10-454-351-2
```

```
Query Match        1.9%;     Score 120.5;  DB 12;  Length 2597;
Best Local Similarity  18.6%;  Pred. No. 0.67;
Matches  145;   Conservative  113;  Mismatches  287;  Indels  233;  Gaps  40;

Qy   416  AGPHLAANPQTD--RDGHVLSSQSTGSSNTE------------FSVDYLALICG  455
Db   274  SGAFLCTKPTIDPSLKSKSLVTQEDNGSASTSPQDFIEPFGSLSLNMTXXSGNKADMVCS  333

Qy   456  FGAPLLARLLFVLERCDAGAFTGGHGDALKYVTGTFDSEIPCSLCEKGHTRPV----CAHT  511
Db   334  IQKP---------SRTSPTAFTEENDYIM--LNASFSTNLVCSVDYNHIQPVWQLLALYS  382

Qy   512  TVHRLRQRMP--------RFGQAIRQPIGVGFTMNSQYSDCDPLGNYAPYLILRKPGD  561
Db   383  DSPLILERKPQLTETPSLSSRYKQVALRPEDIFTSIEADVR-ADPFWFQQEKIVLQLNRT  441

Qy   562  QTEAAKATMQDTYRATLERLFIDLEQERL------------GAPCSSEG  601
Db   442  ATTLISTLQIQFSTDAQIALPRAEMRAERLKWTMILMNNPKLERTVLVGGTIALSCPGKG  501

Qy   602  -----LSSVIVDHPTFR--------RILDTLRARIE-QTTTQFMKVL---VETRD------  639
Db   502  DPSPHLEWLLADGSKVRAPYVSEDGRILIDKNGKLELQMADSFDAGLYHCISTNDADADV  561

Qy   640  --YKIR--EGLSEATHSMALTFDPYSGAF---CPITNFLVKRTHLAVVQDLALSQCHCV  691
```

; LENGTH: 2597
; TYPE: PRT
; ORGANISM: Rattus species
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(2597)
; OTHER INFORMATION: 'x' can be any amino acid
US-10-454-351-13

Query Match   1.9%;   Score 120.5;   DB 12;   Length 2597;
Best Local Similarity   18.6%;   Pred. No. 0.67;
Matches 145;   Conservative 113;   Mismatches 287;   Indels 233;   Gaps 40;

```
                                                                                                 FSVDYLALICG  455
Qy  416 AGPHLAANPQTD---RDGHVLSSQSTGSSNTE-----------------------------  :.|:..    |   ||.|:
Db  274 SGAFLCTKFTIDPSLKSKSLVTQEDNGSASTSPQDFIEFFGSLSNMTXXSGNKADMVCS  333

Qy  456 FGAPLLARLLFYLERCDAGAFTGGHGDALKYVTGTFDSEIPCSLCEKHTRPV----CAHT  511
         ||||||||||||||||||||||||||||||||||||||. :|:.. |:
Db  334 IQKP---------SRTSPFTAFTEENDYIM-LNASFSTNLVCSVDYNHIQPVWQLLALYS  382

Qy  512 TVHRLRQRMP---------RFGQATRQPIGVFGTMNSQYSDCDPLGNYAPYLLIRKPGD  561
         .:|:..    ||
Db  383 DSPLILERKPQLTETPSLSSRYKQVALRPEDIFTSIEADVR-ADPFWFQQEKIVLQLNRT  441

Qy  562 QTEAAKATMQDTYRATLERLFIDLEQERL---------GAPCSSEG  601
         |||                       .:|:.
Db  442 ATTLSTLQIQFSTDAQIALPRAEMRAERLKWTMILMMNNPKLERTVLVGGTIALSCPGKG  501

Qy  602 -----LSSVIVDHPTFR--------RILDTLRARIE-QTTTQFMKVL-----VETRD----  639
           .:. ||
Db  502 DPSPHLEWLLADGSKVRAPYVSEDGRILIDKNGKLELQMADSFDAGLYHCISTNDADADV  561

Qy  640 --YKIR--EGLSEATHSMALTFDPYSGAF----CPITNFLVKRTHLAVVQDLALSQCHCV  691
           .::.                          |||.
Db  562 LTYRITVVEPYGESTHDSGVQHTVVTGETLDLPCLSTG----------VPDASIS---WI  608

Qy  692 FYGQQVEGRNFRNQFQPVLRRRFVDLFNGGFISTRSITVTLSEGPVS--APNPT------  743
         :                                          .:|:.
Db  609 LPGNTVFSQPSRDR--------------QILNNGTLRILQVT-PKDQGHYQCVAANPSGADFSS  657

Qy  744 ------------LGQDAPAGRTFDGDLARVSVEVIRDIRVKNRVVFSGNCTNLSEAARAR  791
                                 :|:.
Db  658 FKVSVQKKGQRMVEHDREAGGSGLGE-PNSSVSLKQPASLK---LSASALTGSEAGKQ-  711

Qy  792 LVGLASAYQRQEKRVDMLHGALG-FLLKQFHGLLFPRGMPPNSKSPNPQWFWTLLQ--R  847
         ||.                                                    ||
Db  712 ----VSGVHRKNKHRDLIHRRGDSTLRRFRE--HRRQLFLSARRIDPQRWAALLEKAKK  765

Qy  848 NQMPADKLTHEITT-------IAAVKRFTEYAAINFINLPPTCIGELAQFYMANLILK  900
          :|:.                         |   |||
Db  766 NSVP----KKQENTTVKPVPLAVPLVELTDEEKDASGMI--PP  802

Qy  901 YCDHSQYLINTLTSIITGARRPRDPSSVLHWIRKDVTSAADIETQAKALLEKTENLPELW  960
                                 ||.:.:|:.
Db  803 --DEEFMVLKTKASGVPGRSPTADSGPVNHGFMTSIASGTEVSTVNPQTLQ-SEHLPDFK  859

Qy  961 TTAFTSTHLVRAAM--------------NQRPMVVLGISISKYHGAAGNNRVFQAGNWSG--  1006
         ||.                        :|:.|||
Db  860 LFSVTNGTAVTKSMNPSIASKIEDTTNQNPIIIFP-SVAEIRDSA------QAGRASSQS  912

Qy 1007 ---LNGGKNVCPLFTFDRTRRFIIACPRGGFI-------------CPVTG--PSSGN  1045
                                                   |||
Db  913 AHPVTCGN---MATYGHTNTYSSFTSKASTVLQPINPTESYGPQIPITGVSRPSSSD  966
```

RESULT 22
US-09-729-485A-2
; Sequence 2, Application US/09729485A
; Publication No. US2002022026A1
; GENERAL INFORMATION:
; APPLICANT: Quark Biotech, Inc.
; APPLICANT: Einat, Paz

RESULT 21
US-10-454-351-13
; Sequence 13, Application US/10454351
; Publication No. US2004005330lA1
; GENERAL INFORMATION:
; APPLICANT: Quark Biotech Inc.; Paz Einat, et al
; TITLE OF INVENTION: GENES ASSOCIATED WITH MECHANICAL STRESS, EXPRESSION PRODUCTS THERE
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 010/PCT2-US2; EINAT=7E
; CURRENT APPLICATION NUMBER: US/10/454,351
; CURRENT FILING DATE: 2003-06-04
; PRIOR APPLICATION NUMBER: US 09/991,630
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 09/905,129
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 09/802,318
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 09/729,485
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: US 09/312,216
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13

```
;   APPLICANT:    Segev, Orbit
;   APPLICANT:    Skaliter, Rami
;   APPLICANT:    Feinstein, Elena
;   APPLICANT:    Faerman, Alexander
;   TITLE OF INVENTION: GENES ASSOCIATED WITH MECHANICAL STRESS, EXPRESSION PRODUCTS THERE
;   FILE REFERENCE: 540579-2007
;   CURRENT APPLICATION NUMBER: US/09/729,485
;   CURRENT FILING DATE: 2000-12-04
;   PRIOR APPLICATION NUMBER: 09/729,485
;   PRIOR FILING DATE: 2000-12-04
;   PRIOR APPLICATION NUMBER: 09/632,862
;   PRIOR FILING DATE: 1998-05-11
;   PRIOR FILING DATE: 2000-08-04
;   PRIOR APPLICATION NUMBER: 60/207,821
;   PRIOR APPLICATION NUMBER: 60/084,944
;   PRIOR FILING DATE: 2000-05-30
;   PRIOR APPLICATION NUMBER: 60/085,673
;   PRIOR FILING DATE: 1998-05-15
;   NUMBER OF SEQ ID NOS: 22
;   SOFTWARE: PatentIn version 3.1
;   SEQ ID NO 2
;   LENGTH: 2597
;   TYPE: PRT
;   ORGANISM: Rattus species
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(2597)
;   OTHER INFORMATION: "Xaa" can be any amino acid
US-09-729-485A-2

Query Match        1.9%;     Score 120.5; DB 12;  Length 2597;
Best Local Similarity   18.6%;   Pred. No. 0.67;
Matches  145;    Conservative 113;   Mismatches  287;   Indels  233;   Gaps  40;

Qy    416  AGPHLAANPQTD--RDGHVLSSQSTGSSNTE---------------------FSVDYLALICG  455
                ||| :|                    ||  |                              ::|
Db    274  SGAFLCTKPTIDPSLKSKSLVTQEDNGSASTSPQDFIEPFGSLSLNMTXXSGNKADMVCS  333

Qy    456  FGAPLLARLLFYLERCDAGAFTGGHGDALKYVTGTFDSEIPCSLCEKHTRPV----CAHT  511
                |||||                    ||| ||        :| |:
Db    334  IQKP---------SRTSPTAFTEENDYIM--LNASFSTNLVCSVDYNHIQPVWQLLALYS  382

Qy    512  TVHRLRQRMP----------RFGQATRQPIGVFGTMNSQYSDCDPLGNYAPYLILRKPGD  561
                :|: |:                    |:| :  |     ::|:
Db    383  DSPLILERKPQLTETPSLSSRYKQVALRPEDIFTSIEADVR-ADPFWFQQEKIVLQLNRT  441

Qy    562  QTEAAKATMQDTYRATLERLFIDLEQERL-------------LDR-----GAPCSSEG    601
                :|                                            |||:
Db    442  ATTLSTLQIQFSTDAQIALPRAEMRAERLKWTMILMNNPKLERTVLVGGTIALSCPGKG  501

Qy    602  ----------LSSVIVDHPTFR---------RIIDTLRARIE-QTTTQFMKVL---VETRD---  639
                                                     :|:  |            ||
Db    502  DPSPHLEWLLADGSKVRAPYVSEDGRILIDKNGKLELQMADSFDAGLYHCISTNDADADV  561

Qy    640  --YKIR--EGLSEATHSMALTFDPYSGAF-----CPITNFLVKRTHLAVVQDLALSQCHCV  691
                    |||                    :||                 :
Db    562  LTYRITVVEPYGESTHDSGVQHVVTGETLDLPCLSTG---------VPDASIS---WI  608

Qy    692  FYGQQVEGRNFRNQFQPVLRRRFVDLFNGGFISTRSIITVTLSEGPVS--APNPT-----  743
                                          |||       :|                 |
Db    609  LPGNTVFSQPSRDR----------QILNNGTLRILQVT-PKDQGHYQCVAANPSGADFSS  657

Qy    744  ----------LGQDAPAGRTFDGDLARVSVEVIRDIRVKNRVVFSGNCTNLSEAARAR  791
                            || |                    |||:
Db    658  FKVSVQKKGQRMVEHDREAGGSGLGE-PNSSVSLKQPASLK----LSASALTGSEAGKQ-  711

Qy    792  LVGLASAYQRQEKRVDMLHGALG-FLLKQFHGLLFPRGMPPNSKSPNFQWFWTLLQ---R  847
                                                            |||
Db    712  -----VSGVHRKNKHRDLIHRRGDSTLRRFRE--HRRQLPLSARRIDPQRWAALLEKAKK  765

Qy    848  NQMPADKLTHEETT-------IAAVKRFTEEYAAINFINLPPTCIGELAQFYMANLILK  900
                 | ||         ||
```

```
Db    766  NSVP----KKQENTTVKPVPLAVPLVELTDEEKDASGMI--PP-------------  802
                                                            ||
Qy    901  YCDHSQYLINTLLTSIITGARRRPDPSSVLHWIRKDVTSAADIETQAKALLEKTENLPELW  960
                                                                    :
Db    803  --DEEFMVLKTKASGVPGRSPTADSGPVNHGFMTSIASGTEVSTVNPQTLQ-SEHLPDFK  859
                                    |: ||
Qy    961  TTAFTSTHLVRAAM----------------NQRPMVLGISISKYHGAAGNNRVFQAGNWSG--  1006
                                                   : :|  |||
Db    860  LFSVTNGTAVTKSMNPSIASKIEDTTNQNPIIFP-SVAEIRDSA------QAGRASSOS  912
                                            ||| |
Qy    1007 ---LNGGKNVCPLFTFDRTRRFIIACPRGGFI----------CPVTG---PSSGN  1045
                     :|:   ||||                          |||||
Db    913  AHPVTGGN---MATYGHNTYSFTSKASTVLQPINPTESYGPQIPITGVSRPSSSD  966
```

```
RESULT 23
US-09-729-485A-10
;   Sequence 10, Application US/09729485A
;   Publication No. US20020022026A1
;   GENERAL INFORMATION:
;   APPLICANT:    Quark Biotech, Inc.
;   APPLICANT:    Einat, Paz
;   APPLICANT:    Segev, Orbit
;   APPLICANT:    Skaliter, Rami
;   APPLICANT:    Feinstein, Elena
;   APPLICANT:    Faerman, Alexander
;   TITLE OF INVENTION: GENES ASSOCIATED WITH MECHANICAL STRESS, EXPRESSION PRODUCTS THERE
;   TITLE OF INVENTION: AND USES THEREOF
;   FILE REFERENCE: 540579-2007
;   CURRENT APPLICATION NUMBER: US/09/729,485A
;   CURRENT FILING DATE: 2000-12-04
;   PRIOR APPLICATION NUMBER: 09/729,485
;   PRIOR FILING DATE: 2000-12-04
;   PRIOR APPLICATION NUMBER: 09/632,862
;   PRIOR FILING DATE: 2000-08-04
;   PRIOR FILING DATE: 2000-08-04
;   PRIOR APPLICATION NUMBER: 60/207,821
;   PRIOR FILING DATE: 2000-05-30
;   PRIOR APPLICATION NUMBER: 60/084,944
;   PRIOR APPLICATION NUMBER: 60/085,673
;   PRIOR FILING DATE: 1998-05-11
;   PRIOR APPLICATION NUMBER: 60/085,673
;   PRIOR FILING DATE: 1998-05-15
;   NUMBER OF SEQ ID NOS: 22
;   SOFTWARE: PatentIn version 3.1
;   SEQ ID NO 10
;   LENGTH: 2597
;   TYPE: PRT
;   ORGANISM: Rattus species
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(2597)
;   OTHER INFORMATION: "Xaa" can be any amino acid
US-09-729-485A-10

Query Match        1.9%;     Score 120.5; DB 12;  Length 2597;
Best Local Similarity   18.6%;   Pred. No. 0.67;
Matches  145;    Conservative 113;   Mismatches  287;   Indels  233;   Gaps  40;

Qy    416  AGPHLAANPQTD--RDGHVLSSQSTGSSNTE-------------------FSVDYLALICG  455
Db    274  SGAFLCTKPTIDPSLKSKSLVTQEDNGSASTSPQDFIEPFGSLSLNMTXXSGNKADMVCS  333
Qy    456  FGAPLLARLLFYLERCDAGAFTGGHGDALKYVTGTFDSEIPCSLCEKHTRV----CAHT  511
Db    334  IQKP---------SRTSPTAFTEENDYIM--LNASFSTNLVCSVDYNHIQPVWQLLALYS  382
Qy    512  TVHRLRQRMP----------RFGQATRQPIGVFGTMNSQYSDCDPLGNYAPYLILRKPGD  561
Db    383  DSPLILERKPQLTETPSLSSRYKQVALRPEDIFTSIEADVR-ADPFWFQQEKIVLQLNRT  441
Qy    562  QTEAAKATMQDTYRATLERLFIDLEQERL-------------LDR-----GAPCSSEG    601
Db    442  ATTLSTLQIQFSTDAQIALPRAEMRAERLKWTMILMNNPKLERTVLVGGTIALSCPGKG  501
```

US-09-729-485A-13

Query Match   1.9%; Score 120.5; DB 12; Length 2597;
Best Local Similarity 18.6%; Pred. No. 0.67;
Matches 145; Conservative 113; Mismatches 287; Indels 233; Gaps 40;

```
Qy    416 AGPHLAANPQTD--RDGHVLSSQSTGSSNTE----------FSVDYLALICG 455
              :::   : :::  :::  :.  : :::::         :::  : :.:::
Db    274 SGAFLCTKPTIDPSLKSKSLVTQEDNGSASTSPQDFIEPFGSLSLNMTKXSGNKADMVCS 333

Qy    456 FGAPLLARLLFYLERCDAGAFTGGHGDALKYVTGTFDSEIPCSLCEKHTRPV----CAHT 511
Db    334 IQKP---------SRTSPTAFTEENDYIM-LNASFSTNLVCSVDYNHIQPVWQLLALYS 382

Qy    512 TVHRLRQRMP------------RFGQATRQPIGVFGTMNSQYSDCDPLGNYAPYLILRKPGD 561
Db    383 DSPLILERKPQLTETPSLSSRYKQVALRPEDIFTSIEADVR-ADPFWFQQEKIVLQLNRT 441

Qy    562 QTEAAKATMQDTYRATLERLFIDLEQERL-----------LDR-------GAPCSSEG 601
Db    442 ATTLSTLQIQFSTDQIALPRAEMRAERLKWTMILMNNPKLERTVLVGGTIALSCPGKG 501

Qy    602 -----LSSVIVDHPTFR--------RILDTLRARIE-QTTTQFMKVL---VETRD- 639
Db    502 DPSPHLEWLLADGSKVRAPYVSEDGRILIDKNGKLELQMADSFDAGLYHCISTNDADADV 561

Qy    640 --YKIR--EGLSEATHSMALTFDPYSGAF----CPITNFLVKRTHLAVVQDLALSQCHCV 691
Db    562 LTYRITVVEPYGESTHDSGVQHTVVTGETLDLPCLSTG----------VPDASIS--WI 608

Qy    692 FYGQQVEGRNFRNQFQPVLRRRFVDLFNGGFISTRSITVTLSEGPVS--APNPT- 743
Db    609 LPGNTVFSQPSRDR---------QILNNGTLRILQVT-PKDQGHYQCVAANPSGADFSS 657

Qy    744 ------------LGQDAPAGRTFDGDLARVSVEVIRDIRVQNRVVFSGNCTNLSEAARAR 791
Db    658 FKVSVQKKGQRMVEHDREAGGSGLGE-PNSSVSLKQPASLK---LSASALTGSEAGKQ- 711

Qy    792 LVGLASAYQRQEKRVDMLHGALG-FLLKQFHGLLFPRGMPPNSKSPNPQWFWTLLQ--R 847
Db    712 --VSGVHRKNKHRDLIHRRRGDSTLRRFRE--HRRQLPLSARRIDPQRWAALLEKAKK 765

Qy    848 NQMPADKLTHEITT----------IAAVKRFTEYAAINFINLPPTCIGELAQFYMANLILK 900
Db    766 NSVP----KKQENTTVKPVPLAVPLVELTDEKDASGMI--PP------- 802

Qy    901 YCDHSQYLINTLTSIITGARRPRDPSSVLHWIRKDVTSAADIETQAKALLEKTENLPELW 960
Db    803 --DEEFMVLKTKASGVPGRSPTADSGPVNHGFMTSIASGTEVSTVNPQTLQ-SEHLPDFK 859

Qy    961 TTAFTSTHLVRAAM----------NQRPMVVLGISISKYHGAAGNNRVFQAGNWSG-- 1006
Db    860 LFSVTNGTAVTKSMNPSIASKIEDTTNQNPIIIFP-SVAEIRDSA------QAGRASSQS 912

Qy   1007 ---LNGGKNVCPLFTFPDRTRRFIIACPRGGFI-----------CPVTG---PSSGN 1045
Db    913 AHPVTGGN---MATYGHTNTYSSFTSKASTVLQPINPTESYGPQIPITGVSRPSSSD 966
```

RESULT 25
US-09-802-318-2
; Sequence 2, Application US/09802318
; Publication No. US20020086825A1
; GENERAL INFORMATION:
; APPLICANT: Einat, et al
; TITLE OF INVENTION: GENES ASSOCIATED WITH MECHANICAL STRESS,EXPRESSION PRODUCTS THEREOF
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 540579-2007.1
; CURRENT APPLICATION NUMBER: US/09/802,318
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 09/632,862
; PRIOR APPLICATION FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/207,821

```
Qy    602 ----LSSVIVDHPTFR--------RILDTLRARIE-QTTTQFMKVL---VETRD----- 639
Db    502 DPSPHLEWLLADGSKVRAPYVSEDGRILIDKNGKLELQMADSFDAGLYHCISTNDADADV 561

Qy    640 --YKIR--EGLSEATHSMALTFDPYSGAF----CPITNFLVKRTHLAVVQDLALSQCHCV 691
Db    562 LTYRITVVEPYGESTHDSGVQHTVVTGETLDLPCLSTG----------VPDASIS--WI 608

Qy    692 FYGQQVEGRNFRNQFQPVLRRRFVDLFNGGFISTRSITVTLSEGPVS--APNPT- 743
Db    609 LPGNTVFSQPSRDR---------QILNNGTLRILQVT-PKDQGHYQCVAANPSGADFSS 657

Qy    744 ------------LGQDAPAGRTFDGDLARVSVEVIRDIRVQNRVVFSGNCTNLSEAARAR 791
Db    658 FKVSVQKKGQRMVEHDREAGGSGLGE-PNSSVSLKQPASLK---LSASALTGSEAGKQ- 711

Qy    792 LVGLASAYQRQEKRVDMLHGALG-FLLKQFHGLLFPRGMPPNSKSPNPQWFWTLLQ--R 847
Db    712 --VSGVHRKNKHRDLIHRRRGDSTLRRFRE--HRRQLPLSARRIDPQRWAALLEKAKK 765

Qy    848 NQMPADKLTHEITT----------IAAVKRFTEYAAINFINLPPTCIGELAQFYMANLILK 900
Db    766 NSVP----KKQENTTVKPVPLAVPLVELTDEKDASGMI--PP------- 802

Qy    901 YCDHSQYLINTLTSIITGARRPRDPSSVLHWIRKDVTSAADIETQAKALLEKTENLPELW 960
Db    803 --DEEFMVLKTKASGVPGRSPTADSGPVNHGFMTSIASGTEVSTVNPQTLQ-SEHLPDFK 859

Qy    961 TTAFTSTHLVRAAM----------NQRPMVVLGISISKYHGAAGNNRVFQAGNWSG-- 1006
Db    860 LFSVTNGTAVTKSMNPSIASKIEDTTNQNPIIIFP-SVAEIRDSA------QAGRASSQS 912

Qy   1007 ---LNGGKNVCPLFTFPDRTRRFIIACPRGGFI-----------CPVTG---PSSGN 1045
Db    913 AHPVTGGN---MATYGHTNTYSSFTSKASTVLQPINPTESYGPQIPITGVSRPSSSD 966
```

RESULT 24
US-09-729-485A-13
; Sequence 13, Application US/09729485A
; Publication No. US20020022026A1
; GENERAL INFORMATION:
; APPLICANT: Quark Biotech, Inc.
; APPLICANT: Einat, Paz
; APPLICANT: Segev, Orbit
; APPLICANT: Skaliter, Rami
; APPLICANT: Feinstein, Elena
; APPLICANT: Faerman, Alexander
; TITLE OF INVENTION: GENES ASSOCIATED WITH MECHANICAL STRESS, EXPRESSION PRODUCTS THERE
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 540579-2007
; CURRENT APPLICATION NUMBER: US/09/729,485A
; CURRENT FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 09/729,485
; PRIOR APPLICATION FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 09/632,862
; PRIOR APPLICATION FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/207,821
; PRIOR APPLICATION FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: 60/084,944
; PRIOR APPLICATION FILING DATE: 1998-05-11
; PRIOR APPLICATION NUMBER: 60/085,673
; PRIOR APPLICATION FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 2597
; TYPE: PRT
; ORGANISM: Rattus species
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(2597)
; OTHER INFORMATION: "Xaa" can be any amino acid

```
Query Match          1.9%;   Score 120.5;   DB 12;   Length 2597;
Best Local Similarity      18.6%;   Pred. No. 0.67;
Matches  145;   Conservative  113;   Mismatches  287;   Indels  233;   Gaps   40;

Qy   416  AGPHLAANPQTD--RDGHVLSSQSTGSSNTE------------------FSVDYLALICG  455
              :  :.  :     :::: ::    ::                   ::.::
Db   274  SGAFLCTKPTIDPSLKSKSLVTQEDNGSASTSPQDFIEPFGSLSLNMTXXSGNKADMVCS  333

Qy   456  FGAPLLARLLFYLERCDAGAFTGGHGDALKYVTGTFDSEIPCSLCEKHTRPV----CAHT  511
              :: .::. :: ::                           .::::
Db   334  IQKP--------SRTSPTAFTEENDYIM--LNASFSTNLVCSVDYNHIQPVWQLLALYS   382

Qy   512  TVHRLRQRMP--------RFGQATRQPIGVFGTMNSQYSDCDPLGNYAPYLILRKPGD  561
              :                :  ::          :: .:
Db   383  DSPLILERKPQLTETPSLSSRYKQVALRPEDIFTSIEADVR-ADPFWFQQEKIVLQLNRT  441

Qy   562  QTEAAKATMQDTYRATLERLFIDLEQERL----------LDR--------GAPCSSEG  601
              ::                :                       :.:
Db   442  ATTLSTLQIFSTDAQIALPRAEMRAERLKWTMILMMNNPKLERTVLVGGTIALSCPGKG  501

Qy   602  ------LSSVIVDHPTFR--------RILDTLRARIE-QTTTQFMKVL---VETRD------  639
              :: :                   ::
Db   502  DPSPHLEWLLADGSKVRAPYVSEDGRILIDKNGKLELQMADSFDAGLYHCISTNDADADV  561

Qy   640  --YKIR--EGLSEATHSMALTFDPYSGAF------CPITNFLVKRTHLAVVQDLALSQCHCV  691
              ::.                               :::::
Db   562  LTYRITVVEPYGESTHDSGVQHTVVTGETLDLPCLSTG------VPDASIS---WI  608

Qy   692  FYGQVEGRNFRNQFQPVLRRRFVDLFNGGFISTRSITVTLSEGPVS--APNPT------  743
              :: :                      :::                 ::
Db   609  LPGNTVFSQPSRDR--------QILNNGTLRILQVT-PKDQGHYQCVAANPSGADFSS  657

Qy   744  --------LGQDAPAGRTFDGDLARVSVEVIRDIRVKNRVVFSGNCTNLSEAARAR  791
                       :: :::                                  :::
Db   658  FKVSVQKKGQRMVEHDREAGGSGLGE-PNSSVSLKQPASLK----LSASALTGSEAGKQ-  711

Qy   792  LVGLASAYQREKRVDMLHGALG-FLLKQFHGLLFPRGMPPNSKSPNPQWFWTLLQ---R  847
              :: :                    :::
Db   712  ----VSGVHRKNKHRDLIHRRRGDSTLRRFRE--HRRQLPLSARRIDPQRWAALLEKAKK  765

Qy   848  NQMPADKLTHEEITT--------IAAVKRFTEEYAAINFINLPPTCIGELAQFYMANLILK  900
              ::                                            :::
Db   766  NSVP-----KKQENTTVKPVPLAVPLVELTDEEKDASGMI--PP-----------  802

Qy   901  YCDHSQYLINTLTSIITGARRPRDPSSVLHWIRKDVTSAADIETQAKALLEKTENLPELW  960
              :::                                        :::
Db   803  --DEEFMVLKTKASGVPGRSPTADSGPVNHGFMTSIASGTEVSTVNPQTLQ-SEHLPDFK  859

Qy   961  TTAFTSTHLVRAAM------------------NQRPMVLGISISKYHGAAGNNRVFQAGNWSG--  1006
```

```
Query Match          1.9%;   Score 120.5;   DB 12;   Length 2597;
Best Local Similarity      18.6%;   Pred. No. 0.67;
Matches  145;   Conservative  113;   Mismatches  287;   Indels  233;   Gaps   40;

Qy   416  AGPHLAANPQTD--RDGHVLSSQSTGSSNTE------------------FSVDYLALICG  455
Db   274  SGAFLCTKPTIDPSLKSKSLVTQEDNGSASTSPQDFIEPFGSLSLNMTXXSGNKADMVCS  333

Qy   456  FGAPLLARLLFYLERCDAGAFTGGHGDALKYVTGTFDSEIPCSLCEKHTRPV----CAHT  511
Db   334  IQKP--------SRTSPTAFTEENDYIM--LNASFSTNLVCSVDYNHIQPVWQLLALYS   382

Qy   512  TVHRLRQRMP--------RFGQATRQPIGVFGTMNSQYSDCDPLGNYAPYLILRKPGD  561
Db   383  DSPLILERKPQLTETPSLSSRYKQVALRPEDIFTSIEADVR-ADPFWFQQEKIVLQLNRT  441

Qy   562  QTEAAKATMQDTYRATLERLFIDLEQERL----------LDR--------GAPCSSEG  601
Db   442  ATTLSTLQIFSTDAQIALPRAEMRAERLKWTMILMMNNPKLERTVLVGGTIALSCPGKG  501

Qy   602  ------LSSVIVDHPTFR--------RILDTLRARIE-QTTTQFMKVL---VETRD------  639
Db   502  DPSPHLEWLLADGSKVRAPYVSEDGRILIDKNGKLELQMADSFDAGLYHCISTNDADADV  561

Qy   640  --YKIR--EGLSEATHSMALTFDPYSGAF------CPITNFLVKRTHLAVVQDLALSQCHCV  691
Db   562  LTYRITVVEPYGESTHDSGVQHTVVTGETLDLPCLSTG------VPDASIS---WI  608

Qy   692  FYGQVEGRNFRNQFQPVLRRRFVDLFNGGFISTRSITVTLSEGPVS--APNPT------  743
Db   609  LPGNTVFSQPSRDR--------QILNNGTLRILQVT-PKDQGHYQCVAANPSGADFSS  657

Qy   744  --------LGQDAPAGRTFDGDLARVSVEVIRDIRVKNRVVFSGNCTNLSEAARAR  791
Db   658  FKVSVQKKGQRMVEHDREAGGSGLGE-PNSSVSLKQPASLK----LSASALTGSEAGKQ-  711

Qy   792  LVGLASAYQREKRVDMLHGALG-FLLKQFHGLLFPRGMPPNSKSPNPQWFWTLLQ---R  847
Db   712  ----VSGVHRKNKHRDLIHRRRGDSTLRRFRE--HRRQLPLSARRIDPQRWAALLEKAKK  765

Qy   848  NQMPADKLTHEEITT--------IAAVKRFTEEYAAINFINLPPTCIGELAQFYMANLILK  900
Db   766  NSVP-----KKQENTTVKPVPLAVPLVELTDEEKDASGMI--PP-----------  802

Qy   901  YCDHSQYLINTLTSIITGARRPRDPSSVLHWIRKDVTSAADIETQAKALLEKTENLPELW  960
Db   803  --DEEFMVLKTKASGVPGRSPTADSGPVNHGFMTSIASGTEVSTVNPQTLQ-SEHLPDFK  859

Qy   961  TTAFTSTHLVRAAM------------------NQRPMVLGISISKYHGAAGNNRVFQAGNWSG--  1006
Db   860  LFSVINGTAVTKSMNPSIASKIEDTTNQNPIIIFP-SVAEIRDSA------QAGRASSQS  912

Qy  1007  ---LNGGKNVCPLFTFDRTRRFIIACPRGGFI-------------CPVTG---PSSGN  1045
Db   913  AHPVTGGN----MATYGHTNTYSSFTSKASTVLQPINPTESYGPQIPITGVSRPSSSD  966
```

```
Db    712  ---VSGVHRKNGHRDLIHRRRGDSTLRRFRE--HRRQLPLSARRIDPQRWAALLEKAKK  765
                 |:       |     ||        |:        ||||
Qy    848  NQMPADKLTHEEITT------IAAVKRFTEEYAAINFINLPPTCIGELAQFYMANLILK  900
               :|:     ||     ::     ||      :     |:    ::
Db    766  NSVP----KKQENTVKPVPLAVPLVELTDEEKDASGMI--PP---------------  802
               ::|      ||||     |||      ||
Qy    901  YCDHSQYLINTLTSIITGARRPRDPSSVLHWIRKDVTSAADIEQAKALLEKTENLPELW  960
                 ||||     :|:|    ::||:
Db    803  --DEEFMVLKTKASGVPGRSPTADSGPVNHGFMTSIASGTEVSTVNPQTLQ-SEHLPDFK  859
               :|:|    ||||        ||      :|:|
Qy    961  TTAFTSTHLVRAAM----------NQRPMVVLGISISXYHGAAGNNRVFQAGNWSG--  1006
               |:|:     ||||      :|||:::     ::|
Db    860  LFSVTNGTAVTKSMNPSIASKIEDTTNQNPIIIFP-SVAEIRDSA-----QAGRASSQS  912
               |||||||||||||||||||||||||||||||||  |||||||||      |||||||||
Qy   1007  ---LNGGKNVCPLFTFDRTRRFIIACPRGGFI---------------CPVTG---PSSGN  1045
                     :|: | ||||      :|||      |||||      ||||     |||||
Db    913  AHPVTGGN---MATYGHTNTYSSFTSKASTVLQPINPTESYGPQIPITGVSRFSSSD  966
                   ||||      |||||||||||||||||||||||||||||||||||||||||||
```

```
RESULT 27
US-09-802-318-13
; Sequence 13, Application US/09802318
; Publication No. US20020086825A1
; GENERAL INFORMATION:
;  APPLICANT: Einat, et al
;  TITLE OF INVENTION: GENES ASSOCIATED WITH MECHANICAL STRESS, EXPRESSION PRODUCTS THERE
;  TITLE OF INVENTION: AND USES THEREOF
;  FILE REFERENCE: 540579-2007.1
;  CURRENT APPLICATION NUMBER: US/09/802,318
;  CURRENT FILING DATE: 2001-03-08
;  PRIOR APPLICATION NUMBER: 09/632,862
;  PRIOR FILING DATE: 2000-08-04
;  PRIOR APPLICATION NUMBER: 60/207,821
;  PRIOR FILING DATE: 2000-05-30
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
;  LENGTH: 2597
;  TYPE: PRT
;  ORGANISM: Rattus sp.
;  FEATURE:
;  NAME/KEY: misc_feature
;  LOCATION: (1)..(2597)
;  OTHER INFORMATION: 'x' can be any amino acid
US-09-802-318-13

Query Match             1.9%;  Score 120.5; DB 12; Length 2597;
Best Local Similarity  18.6%;  Pred. No. 0.67; 
Matches  145;  Conservative 113;  Mismatches 287;  Indels 233;  Gaps 40;
```

```
Qy    416  AGPHLAANPQTD---RDGHVLSSQTGSSNTE-----------------FSVDYLALICG  455
                  :|||       ::|:|      ||::|             ::
Db    274  SGAFLCTKPTIDPSLKSKSLVTQEDNGSASTSPQDFIEPFGSLSLNMTXXSGNKADMVCS  333
                  |  |||| |:      ||      :||        ||
Qy    456  FGAPLLARLLFYLERCDAGAFTGGHGDALKYVTGTFDSEIPCSLCEKHTRPV---CAHT  511
                  ||:||      :||      ::::|    ||      :|||     :
Db    334  IQKP--------SRTSPTATEENDYIM--LNASPSTNLVCSVDYNHIQPVWQLLALYS  382
                  |:|        ::        ::|      |:|    ::||
Qy    512  TVHRLRQRMP----------RFGQATRQPIGVFGTMNSQYSDCDPLGNYAPYLILRKPGD  561
                  |:        :|||      :|:||    ||:|    ||
Db    383  DSPLILERKPQLTETPSLSSRYKQVALRPEDIFTSIEADVR-ADPFWFQQEKIVLQLNRT  441
                   |:||      :||     |:|||      ||||
Qy    562  QTEAAKATMQDTYRATLERLFIDLEQERL----------LDR------GAPCSSEG  601
                  |::       |:|     |::     |||      :|||||
Db    442  ATTLSTLQIQFSTDAQIALPRAEMRAERLKWTMILMNNPKLERITVLVGGTIALSCPGKG  501
                  |:       :|      ||     ::||||
Qy    602  ----LSSVIVDHPFFR-------RILDTLRARIE-QTTTQFMKVL---VETRD------  639
                  ||     :| ||         ||:||     ::|||      :
Db    502  DPSPHLEWLLADGSKVRAPYVSEDGRILIDKNGKLELQMADSFDAGLYHCISTNDADADV  561
                  |:||      ::|    ||||      |:|
Qy    640  --YKIR---EGLSEATHSMALTFDPYSGAF---CPITNFLVKRTHLAVVQDLALSQCHCV  691
                  :|||      :|:|     :|||     ||:
Db    562  LTYRITVEPYGESTHDSGVQHTVVTGETLLDLPCLLSTG-------VPDASIS---WI  608
                  |:||      :||       ||:|:|
Qy    692  FYGQQVEGRNFRNQFQPVLRRRFVDLFNGGFISTRSITVTLSEGPVS--APNPT------  743
                  ||:|      ::|||      :|:|      :|||
Db    609  LPGNTVFSQPSRDR-----------QILNNGTLRILQVT-PKDQGHYQCVAANPSGADFSS  657
                  ||||      :||      ::||
Qy    744  ----------LGQDAPAGRTFDGDLARVSVEVIRDIRVKNRVVFSGNCTNLSSAARAR  791
                  :||      ||:|:|      |:||
Db    658  FKVSVQKKGQRMVEHDREAGGSGLGE-PNSSVSLKQPASLK---LSASALTGSEAGKQ-  711
                  |:||      ::|      :||
Qy    792  LVGLASAYQREKRVDMLHGALG-FLLKQFHGLLFPRGMPPNSKSPNPQWFWTLLQ--R  847
                  |:||      :|:       ||||
```

```
Db    860  LFSVTNGTAVTKSMNPSIASKIEDTTNQNPIIIFP-SVAEIRDSA-----QAGRASSQS  912
                  |||||||||||||||||||||||||||||||||||  ||||||||||      ||||||||
Qy   1007  ---LNGGKNVCPLFTFDRTRRFIIACPRGGFI---------------CPVTG---PSSGN  1045
                     :|:| ||||      :|||      |||||      |||||     |||||
Db    913  AHPVTGGN---MATYGHTNTYSSFTSKASTVLQPINPTESYGPQIPITGVSRFSSSD  966
                   ||||     |||||||||||||||||||||||||||||||||||||||||||
```

```
RESULT 28
US-10-329-079-11
; Sequence 11, Application US/10329079
; Publication No. US20030198981A1
; GENERAL INFORMATION:
;  APPLICANT: FARNET, Chris
;  APPLICANT: ZAZOPOULOS, Emmanuel
;  APPLICANT: STAFFA, Alfredo
;  TITLE OF INVENTION: GENES AND PROTEINS INVOLVED IN THE BIOSYNTHESIS OF LIPOPEPTIDES
;  FILE REFERENCE: 3002-11US
;  CURRENT APPLICATION NUMBER: US/10/329,079
;  CURRENT FILING DATE: 2002-12-24
;  NUMBER OF SEQ ID NOS: 66
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
;  LENGTH: 5245
;  TYPE: PRT
;  ORGANISM: Streptomyces fradiae
US-10-329-079-11

Query Match             1.9%;  Score 120; DB 14; Length 5245;
Best Local Similarity  20.2%;  Pred. No. 2.6; 
Matches  262;  Conservative 138;  Mismatches 434;  Indels 464;  Gaps 68;
```

```
Qy    102  PSSAAPNLTRACNAARERFGFSRCOGPP----VDGAVETTGAEICTRL-----GL  147
                  |:||      |:|       :::|      ||:|
Db    464  PAAAEPAADEGLEAVCDTFARQAAATPEAPAVVCGPVALTFAEADARVSRLARLLISRGA  523
                  |:||      :||      ::||      ::||
Qy    148  EPENTILYLVVTALFKEAVFMCNVFLHYGGLDIVHINHGDVIRIPLFPVQLFMPDVNRLV  207
                  |:||      :|:|      |:|      :||
Db    524  GPE-----VRVAVCLDRNALWPTTV--------LAVLRSGAVHVPL----------  556
                   |||      :||      ||||
Qy    208  PDPFNTHHRSIGEGEVPYPTPFYNTGLCHLLHDCVIAPMAVALRVRNVTAVARGAAHLAF-  266
                   |:||      ::|      |:|      :|||
Db    557  -DPRSPHER-------------LAAVERD--VAPLLVLAERATEAAVADLAAPVLVL  597
                  :|||      ::|       |:|
Qy    267  -DENHEGAV-------------LPPDITYFYFQSSSSG---TTTARG------A  297
                   :||      ::|      ||||
Db    598  DDPSTEAAIDALDPGPVTDADRTAPLLPGHAAYVIHTSGSTGRPKGVTVDHRGLSRLLQA  657
                  |:||      :|:      :||
Qy    298  RRNDVNSTSKPSPSG-GFERRLASI---------------MAADTALHA-----  330
                  ||:|      :|:      ||||
Db    658  HRRVTFSRIRPSAGGPGRAAHVSSFSPDASWDPLLAMVAGHELMIDEDLRFDPPGVVAY  717
                  |:||      ::|      :|||
Qy    331  -------------EVIFNTGIYEE---DIKEWPMFIGMEGTLPRLNAL  365
                   ||||      ::|      |:|
Db    718  FRDRRIDYVDLTPTYFRSLLDAGLLEEGFCPSLVALGGEAMDGELWERLRAAAPRVTAM  777
                  |:||      :|:      ||||
Qy    366  GSY-----TARVA-------GVIGAMVFSPNSALYLTEVEDSGMTEAKDGGPGPSFNR  411
                  |:||      :||      ::||
Db    778  NTYGPTETAVDAVVTVLGDLPPGTIGRPV---PRWRAY---VLDAGLRPVPPGVLGELY-  830
                  |:||      :|:      ||||
Qy    412  FYQFAGPHLAANPQTDRDGHVLSSQSTGSSNTEFSVDYLALICGFGAP-----LLAR  463
                  |:|||      :|:      ::||
```

```
CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 71520
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFL573270E12_FLI.pep
US-10-425-114-71520

Query Match             1.9%;  Score 118;  DB 12;  Length 452;
Best Local Similarity  22.7%;  Pred. No. 0.052;
Matches   91;  Conservative  36;  Mismatches 132;  Indels 142;  Gaps  22;

Qy  195  PVQLFMPDVNRLVPDPFNTHHRSIGEGFVYPTPFYNTGLCHLIHDCVIAPMAVALRVRNV 254
              |||       |  ||             :|:|:||||||  |:|:
Db   90  PVQRWRPVSTEAVPQ----HH---QDDIIETS--NSGSKKIIEDCI------------ 126

Qy  255  TAVARGAAHLAFDENHEGAVLPPDITYTYFQSSSSGTTARGARRNDVNSTSKPSPSG-- 312
                                |||                |||
Db  127  ---------ASEN-----LPPD--------GTTNVVEVTANDASSSKNNLSFGYS 160

Qy  313  ---------GPERRLA----------SIMAADT----- ALHAEVIFNT 336
                  |||||:|            :||||:
Db  161  STKVIEDHAELSGFNKDLAGSNVFGTHSSSVEAVQSRQLDYSHFISLPLALHPDLVNKL 220

Qy  337  GIYEETPTDIKEWPMFIGMEGTLPRLNALGSYTARVAGVIGAMVFSPNSALYLTEVEDSG 396
                  :    :|:         ::|
Db  221  NYFQSS-----ILGEENS-----NKDGSQS--EGSIGEMDY------------DHK 252

Qy  397  MTEAKDGGPGPSFNRFYQ---FAGP---HLAA------NPQTDRDGHVLSQST----G 439
              |    :||           |||
Db  253  QAEAKMGAKGSQSDFGIDKSIFKPETFHLTVLMLKLWNKERIDKASDVLQSVSTQVNEA 312

Qy  440  SSNTEFSVDYLALICGFGAPLLARLLFYLERCDAGAFTGGHGDALKVTGTFDSEIPCSL 499
                     |:          :   ::     |:
Db  313  LENRPISIQLRGLTCMKGFPAKARVV-YVPVLEVGS-EGRLAHACKVITDAF---IKAGL 367

Qy  500  C-EKHTRPVCAHTTVHRLRQRMPRFGQAT----RQPIGVFG 535
            :|  |      ||:      |
Db  368  VFERDVRELKLHATVMNVRHRKSRNKRNTWTDSFDARGIFG 408


RESULT 30
US-10-084-846A-8
; Sequence 8, Application US/10084846A
; Publication No. US2004006026A1
; GENERAL INFORMATION:
; APPLICANT: WEITNAUER, GABRIELE
; APPLICANT: MUHLENWEG, AGNES
; APPLICANT: TREFZER, AXEL
; APPLICANT: BECHTHOLD, ANDREAS
; TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
; FILE REFERENCE: 1974-005
; CURRENT APPLICATION NUMBER: US/10/084,846A
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: PCT/EP01/09815
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: DE 101 09 166.4
; PRIOR FILING DATE: 2001-02-25
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 8
; LENGTH: 19608
; TYPE: PRT
; ORGANISM: Streptomyces viridochromogenes
; FEATURE:
; OTHER INFORMATION: Protein 3: amino acid sequence encoded by coding strand 1.
; OTHER INFORMATION: Start codon: atc, Start position: nucleotide 3.
US-10-084-846A-8

Query Match             1.9%;  Score 118;  DB 15;  Length 19608;
```

```
Db   831  --LAGPGVARGYLGQ--HALTAER------FVACPPGKPGBRMYRTGDLAR 871
Qy   464  L-----LFYLERCD--------AGAF-----TGGHGDALKYV 487
Db   872  WLPDGHLVVGRGDEQVKIRGFRIEPGEVEAALRELEGVAAAAVTVREDTPGTRRLVGYV 931
Qy   488  TGTFDSEIPCSLCEKHTRPVCAHTTVHRLRQRMP-----RFGGQATRQPIGVFGTMNSQY 541
Db   932  VGTPDAD------DARLRPA--EVLARLRDRLPDHLVPSAFVLRELPVNTSGKLDRA- 981
Qy   542  SDCDPLGNYAPYLILIRKPGDQTEAAKATMQDTYRATLERLFIDLEQERLLDRGAPCSSEG 601
Db   982  --ALPAPDPADFPPAGRRP--------RTALEREVCALFAEVL---------G 1014
Qy   602  LSSVIVDHPTFRRILDTLRARIEQTTTQFMKVLVETRDYKIREGLSEATHSMALTFPDYS 661
Db  1015  AGSVGIDDDFFGRGGDSILS------IQLVGSAR---RAGL--TFTVRQVFELRT 1058
Qy   662  GAFCPITNFLVKRTHLAVVQDLALSQCHCVFYGQQVEGRNFRNQFQPVLRRRFVDLFNGG 721
Db  1059  PAALAAA--ARRTDAAGDEDPALA-------VGP-----LPLLPVVAETLAAGG 1098
Qy   722  FISTRSIITVTLSEGPVSAPNPTLGQDAPAGRTFDGDLARVSVEV-----IRDIRVKNR- 774
Db  1099  PVHSYNQSVVLASPPDAAPDDV--RDALQALDRHDALRVHAAPAAGPGRLWDLRVEEAG 1156
Qy   775  VVFSGNC-------TNLS--EAARARLVGLASAYQRQEKRVDMLHGALGFLLKQFHGLLFP 826
Db  1157  TVAAERCLRRIDATGMSDEELARAQAABAVTA---RACLDPLAGAL------VSAVWFD 1206
Qy   827  RGMPP---------NSKSPNPQW--------FWTLLQRNQMPADKLTHEEITTIAAVKRF 869
Db  1207  RGDRPGRLVLVIHHLAVDGVSWRILLGDLREAWRALRAGRRPELPRTGTSLRTWAT--RL 1264
Qy   870  TEBYAAINFINLPPTCIGELAQFYMANLLKYCDHSQYLINTLTSIITGARRPRD-PSS- 927
Db  1265  TERAT------DPAVTAQL-DHWTATLADGPAPGSRPLDRTRDTVATSAVLSGELPASL 1316
Qy   928  --------VLHWI-RKDVTSAADIBTQAKALLEKTENL---- 956
Db  1317  TTDLLGPAPAAFRAGVNDLLLTAFALAVAHWRGEEDAPVLVDLESHG---RTEELVFG 1371
Qy   957  PELWTTA--FTSTHLVRAAMNQRPMVVLGISISKYHGAAGN------NRVFQAGNWSGLNG 1009
Db  1372  ADLSRTVGWFTSVHPVRLAAGR----VTAADLAERRAPAVGDAIKRIKEQLRAVPDGGLGH 1427
Qy  1010  G--KNVCP--------LFTFDRTRRFIIACPRGGFPICPV--TGPSSGNRETTLSDQ 1053
Db  1428  GLLRHLNPDTAPRLRGLARARFGFNYLGRPAAEQGAGEDSWPLLGSGPAGQHPDTPLDHE 1487
Qy  1054  VRGIIVS----GGAMVQLAIYATVVRAVGARAQHMAFDDWLSLTDDEFLARDLEELHDQ 1108
Db  1488  IEVNVVTAEGPDGPRLIITRWTYATGL-----------LTEEE---------- 1518
Qy  1109  IIQTLETPWTVEGALEAVKILDEKTTAG-DGETPTNLA 1145
Db  1519  -VRRLTRSWSL--ALHAV--VGHATAEGAGGLSPSDVA 1551


RESULT 29
US-10-425-114-71520
; Sequence 71520, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
```

```
Db    12590 CVQDAWPSAVGCSVRR---SVRSTMSLMVGSFQKMLAGTS----------RPRRF------- 12631

Qy    1033 GFICPVTGPSSGNRETLSDQVRGIIVSGAMVQLAIYATVVRAVGARAQHMAFDDWLSL 1092
                |||:                                          :|:|
Db    12632 --------SSRRRTTVITESSPCSTSG---------RRTCRAVGASRISCAI----CSR 12670
                                                             |||
Qy    1093 TDDEFLARDLEELHDQIIQTLETPWTVEGALEAVKILDEKTTAGDGETPTNLAFNFDSCE 1152
                                                                      ::::|
Db    12671 TSSS-----------------------------------------TRERSSSGD----- 12684
                                                                            |
Qy    1153 PSHDTTSNVLNISGSNISGS 1172
               |::|||
Db    12685 PANDTTSASASPPGSSVSGA 12704
```

```
RESULT 31
US-10-231-956A-325

; Sequence 325, Application US/10231956A
; Publication No. US2004005233A1
; GENERAL INFORMATION:
;  APPLICANT: Lorens, James B.
;  APPLICANT: Xu, Weiduan
;  APPLICANT: Bogenberger, Jakob
;  APPLICANT: Holland, Sacha
;  APPLICANT: Rigel Pharmaceuticals, Incorporated
;  TITLE OF INVENTION: Modulators of Angiogenesis
;  FILE REFERENCE: 021044-0041000US
;  CURRENT APPLICATION NUMBER: US/10/231,956A
;  CURRENT FILING DATE: 2001-08-30
;  NUMBER OF SEQ ID NOS: 522
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 325
;  LENGTH: 1479
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-10-231-956A-325

  Query Match             1.8%;  Score 114.5;  DB 12;  Length 1479;
  Best Local Similarity  18.5%;  Pred. No. 0.97;
  Matches  204;  Conservative 118;  Mismatches 441;  Indels 341;  Gaps 47;
```

```
Qy    162 FKEAVFMCNVFLHYCGLDIVHINHGDVIRIPLFFVQLFMPD--VNRLVPDFNTHHRSIG 219
              :|:|:           ||:  ::           |||  :        |:
Db    130 FKGLASLEQLHFNQIET--LDPDSFQHLPKLE-RLFLHNNRITTHLVPGTFN-HLESMK 185

Qy    220 EGFVYPTPFYNTGLCHLIHDCVIAPMAVALRVRNVTAVARGAAHLAFDENHEGAVLPPDI 279
                ::                                                |:
Db    186 RLRLDS------NTLHC---DCEILWLADLLKTYAESGNAQAAAICEYPRR--------- 227

Qy    280 TYTYFQSSSGTTARGARRNDVNSTSKPSPSGGFERRLASIMAADTALHAEVIFNTGIY 339
                                                              ::
Db    228 ----IQGRSVATITPELNCERPRITSEPQ--------------------DADVTSGNTVY 264

Qy    340 EETPTDIKEWPMFIGMEG---------------TLPRLNAL----------GSYTARVAGVIG 377
                 |:                                       :|
Db    265 FTCRAEGNPKPEIIWLRNNNELSMKTDSRLNLLDGTLMIQNTQETDQGIYQCMAKNVAG 324

Qy    378 AMVFSPNSALYLTEVEDSGMTEAKDGGPGPSFNRFYQFAGPHLAANPQTDR----DGHVL 433
              :                                                       :
Db    325 ----------EVKTQEVTLRYFGSP-------------ARPTFVIQPQNTEVLVGESVTL 361

Qy    434 SSQSTG---------SSNTEFSVDYLALICGFGAPLLARLLFYLERCDAGAFTGGHGDA 483
                :                             ::
Db    362 ECSATGHPPPRISWTRGDRITPLPVDPRVNITPSGG-------LYIQ----NVVQGDSGEY 410

Qy    484 LKYVTGTFDSEIPCSLCEKHTRPVCAHTTVHRLRQRMPRFGQATRQPIGVFG-TMNSQYS 542
                 :                                              ::
Db    411 ACSATNNIDS------------VHATAFIIVQALPQFTVTPQDRVVIEGQTVFDQ-- 453

Qy    543 DCDPLGNYAPYLILRKPGDQTEAAAKATMQDTYRATLERLFIDLEQERLLDRGA-PCSSEG 601
              ::                                              :
Db    454 -CEAKGNPPPVIAWTKGGSQLSV------DRRHLVLSSGTLRISGVALHDQGQYECQAVN 506
```

(Left column)

```
  Best Local Similarity  19.7%;  Pred. No. 44;
  Matches 240;  Conservative 133;  Mismatches 443;  Indels 404;  Gaps 62;

Qy    106 APNLTRACNAARERFGFSRC--QGPPVDGAVETTGAE------ICTRLGLEP-------- 149
              |||:                                         :||
Db  11736 APHRSPTRTGARPRGHARRCRRGRGRGPIPGA---RGAEPPHASSRLRRSPDSAPSNLL 11792

Qy    150 ---ENTILYLVVTALFKEAVFMCNVFLHYCGLDIVH--INHGD---------VIRIPLFP 195
                                                                    |
Db  11793 ENLENNAKQRIRSAKGKPA--------------GGLSPSHGCCRHGQSHAVGQRALVQRLPPVP 11842

Qy    196 VQLFMPD-----------------------VNRLVPDFNTHHRSIGEGFVY-PTPFYNT 231
              :                                                 ::
Db  11843 V-LGVPAHGVGEALLERHTGCVAERAEAGVAQRVAPVV-----SLPVGVTLDPVPAGAQ 11895

Qy    232 GLCHLIHDCVIAPMAVALRVRNVTAVARGAAHLAFDENHE------GAVLP-PDITYTYFQ 285
              |:|                               :|:      :|:
Db  11896 GVQQLLRQFQIGQLG---RARDVVDLPR---QPAFGDQDPAPHVVGVHVPVDVAAIPVQ 11949

Qy    286 SSSSGTTTARGARRNDVNSTSKPSPSGGFERRLAS--IMAADTALHAEVIFNTGIYEETP 343
                                                    :
Db  11950 RDAVAVQQPGGEQRNDL------------LRELIGPVVVAAPRHAHRQ----------- 11985

Qy    344 TDIKEWPMFIGMEGTLPRLNA-LGSYTARVAG------------VIGAMVFSPNSA 386
              :|:                :                       ::   |
Db  11986 -------PMGAGV-GEGDHVAARLGRRVGRVGGDRRVLVPGARLDAAVHLVGGDLHDPGRA 12038

Qy    387 --LYJTEVEDS---GMTEAKDGGPGPSFNRFYQ--------FAGPHLAANPQTDRDGHVLS 434
                ::|::                                      ||
Db  12039 GLQAHLHECLDALHIG'YERRRVGDRPVDVRFGREVDHQIVAGDHLGEQPGI-ADVAVHE 12097

Qy    435 SQSTGSSNTEFSVDYLALICGFGAPLLARLLFYLERCDAGAFTGGHGHDALKYVTG----- 489
                                                         :
Db  12098 GVPAGDRLQVRQVPVGVGQLVQGHPRRIAV------------PDQFAHVLGADEAR 12141

Qy    490 -TFDSEIPCSLCEKHTRPVCAHTTVHRLRQMPRFGQATROPIGVFGTMNSQYSDCDPLG 548
              ::|                   |:          :|::                |||
Db  12142 STDDQDVPSPF--RTRAAVSHVPVSRLHRRVPSRLHRRVPRLRRPVQPPTWT-RLWSPSTSRCAVDV 12197

Qy    549 NYAPYLILRKPGDQTEAAAKATMQDTYRATLERLFIDLEQERLLD---RGAPCSSEGLSS 604
                    ::                                           :|::
Db  12198 RGAAFTSVSRPITESSTRATPSIEAPRSTIE-YWISLCATRQLPSMEVKGPRESCTTVSG 12256

Qy    605 VIVDHPTFRR---------ILDTLR---ARIEQTTQFMKVLVETRDYKIREGLSEATHSMA-- 654
              :|                                              ::  ::
Db  12257 PMTAGP'MREPEIFAPASTTTRPTSSLASSTSPSMRV---SRDSSRCRFISRTSVTLATS 12313

Qy    655 ------LTPDYSGAFCPITNFLVKRTHLAVVCDLALLSQCHCVFYGGQVEGRNFRNQ---- 705
                                                            ::
Db  12314 FQYRSITVEPTS---CP--------------WSASHC---RASVISSSFRQDGRMP 12349

Qy    706 ------FQPVLRRRFVDLFNGGFISTRSITTVTLSEGPVSAPNPTL-GQDAPAGRT 753
                  ::                                          :::
Db  12350 ATASCTAELKAYTPTIARSL---LGSWGF-STTAVTRPFSS---SSATPNLRGSATRASMT 12403

Qy    754 FDGDLAR---VSVEVIRDIRVKNRVVFSGNCTNLSEARARARIVGLASAYQREKRVDMLH 810
              ::                                              ::
Db  12404 CAAGLSRRKSA'ATKSTMPSTTLSPRYM----TKSSSPRKSRDTSTASASPR-------- 12449

Qy    811 GALGFLLKQFHGLLFPRGMPPNSKSPNPQWFW-------TLLQRNQMPADKL--THEBIT 861
              ::                                          |::
Db  12450 GASCWMVTS---------RPNS-APSPTEAWISAAVAPTTIPTSDIPAS-LMESSTERTV 12498

Qy    862 TIAAVKRFTEBYAAI--NFINLPPTCIGELAQFYMANLILKYCDHSQYLINTLTSIITGA 919
              ::                                             :|
Db  12499 LLATGTSCLAEVCVIGRSLEPITPT-----------NMSAFISHTLRSA---- 12536

Qy    920 RPRPDPSSVLHWIRKDVTSAADIETQAKALLEKTENLPELWTTAFTSTHLVRAAMNQRPM 979
                                                              ||
Db  12537 ------PSDQV--VSRBLQMASNVSAQQRSYWRFVQVFPRFPGRLARPFHPAVPCHELRSQ 12589

Qy    980 VV------LGISISKYHGAAGNNRVFQAGNWSGLNCGGKNVCPLFTPDRTRRFIIACPRG 1032
              |                                              :
```

; ORGANISM: Homo sapiens
US-10-211-462-87

Query Match   1.8%; Score 114.5; DB 12; Length 1496;
Best Local Similarity 18.5%; Pred. No. 0.99;
Matches 204; Conservative 118; Mismatches 441; Indels 441; Gaps 47;

```
Qy  162 FKEAVPMCNVFLHYGGLDIVHINHGDVIRIPLFPVQLFMPD--VNRLVPDDFPNTHRSIG 219
Db  147 FKGLASLEQLYHFNQIET-LDPDSFQHLPKLE-RLFLHNNRITHLVPGTFN-HLESMK   202
Qy  220 EGFVYPTPFYNTGLCHLIHDCVIAPMAVALRVRNTVAVARGAAHLAPDENHEGAVLPPDI 279
Db  203 RLRLDS---NTLHC--DCBILWLADLLKYAESSNAQARAICEYPRR------------   244
Qy  280 TYTYFQSSSGTTARGARRNDVNSTSKPSPSGGFERRLASIMAADTALHAEVIFNTGIY   339
Db  245 ----IQGRSVATITPEELNCERPRITSEPQ------------DADVTSGNTVY         281
Qy  340 EETPTDIKEWPMFIGMEG------TLPRLNAL-----GSYTARVAGVIG           377
Db  282 FTCRAEGNPKPEIIWLRNNNELSMKTDSRLNLLDDGTLMIQNTQETDQGIYQCMAKNVAG 341
Qy  378 AMVFSPNSALYLTEVEDSGMTEAKDGGPGPSFNRFYQFAGPHLAANPQTDR----DGHVL 433
Db  342 ------------EVKTQEVTLRYFGSP-----------ARPFFVIQPQNTEVLVGESVTL 378
Qy  434 SSQSTG------SSNTEPFSVDYLALICGFGAPLLARLLFYLERCDAGAFTGGHGDA     483
Db  379 ECSATGHPPPRISWTRGDRTPLPVDPRVNITPSGG------LYIQ---NVVQGDSGEY   427
Qy  484 LKYVTGTFDSEIPCSLCEKHTRPVCAHTTVHRLRQRMPRFGQATRQPIVFG-TMNSQYS  542
Db  428 ACSATNNIDS------------------VHATAFIIVQALPQFTVTPQDRVVIEQTVDFQ-- 470
Qy  543 DCDPLGNYAPYLILRKPGDQTEAAKATMQDTYRATLERLFIDLEQERLLDRGA-PCSSEG 601
Db  471 -CBAKGNPPVIAWTKGGSQLSV------DRRHLVLSSGTLRISGVALHDQGGYECQAVN   523
Qy  602 L--SSVIVDHPTFRRILDTLRARIEQTTTQFMKVLVETRDYKIREGLSEATHSMALTFDP 659
Db  524 IIGSQKVVAHLTVQPRVTPVFASIPSDT------VEVGANVQLPCSSQGEPEPAITWNK  577
Qy  660 YSGAFCPITNFLVKRTHLAVVQDLA------LSQCHCVFYGQQVEGRNF-RNQFQPVLRRRF 714
Db  578 DGVQVTESGKFHISPEGFLTINDVGPADAGRYECV------ARNTIGSASVSMVLSVNV  630
Qy  715 VDLFNGG--FIST------RSITVT---LSEGPVSAPNTLG------QDA          748
Db  690 PDVSRNGDFVATSIVEAIATVDRAINSTRTHLFDSRPRSPNDLLALFRYPRDPYTVEQA  690
Qy  749 PAGRTFDGDLARVSVEVIRDIRVK------NRVVFSGNCTNLSEAARAR           791
Db  745 RAGEIFERTLQLIQEHVQHGLMVDLNGTSYHYNDLVSPQYLNLIANLSGCT------AHRR 745
Qy  792 LVGLASAYQRQEKRV------DMLHGALGFLLKQFHGLL------PPRGMPPN---    832
Db  805 VNNCSDMCFHQKYRTHDGTCNNLQHPMWGASLTAFERLLKSVYENGFNTPRGINPHRLYN 805
Qy  833 ------SKSPNPQWFWTLLQRNQMPADKLTHEBITTIAAVK--RFTEE            872
Db  861 GHALPMPRLVSTTLLIGTETVTPDEQFTHMLMQWGQF---LDHDLDSTVVALSQARFSDG 861
Qy  873 YAAINFINLPPTCI------GELAQFYMANLILKYCDHSQYLINTLTSIITGA       919
Db  913 QHCSNVCSNDPPCFSVMIPNDSRARSGARCMFVRS------SPVCGSGMTSLLMNS    913
Qy  920 RRPRDPSSVLHWIRKDVTSAADIETQAKALLEKTENLPELWTTAFTSTH--LVRAAMNQR 977
Db  960 VYPREQINQL------TSYIDASNVYGSTEHEARSIRDL------ASHRGLLRQGIVQR  960
Qy  978 PMVVLGISISKYHGAAGNNRVFQAGNWSGLNGGKNVCPLFTFDRTRRFIIACPR----GG 1033
```

Second alignment block:

```
Qy  602 L--SSVIVDHPTFRRILDTLRARIEQTTTQFMKVLVETRDYKIREGLSEATHSMALTFDP 659
Db  507 IIGSQKVVAHLTVQPRVTPVFASIPSDT------VEVGANVQLPCSSQGEPEPAITWNK  560
Qy  660 YSGAFCPITNFLVKRTHLAVVQDLA------LSQCHCVFYGQQVEGRNF-RNQFQPVLRRRF 714
Db  561 DGVQVTESGKFHISPEGFLTINDVGPADAGRYECV------ARNTIGSASVSMVLSVNV  613
Qy  715 VDLFNGG--FIST------RSITVT---LSEGPVSAPNTLG------QDA          748
Db  614 PDVSRNGDFVATSIVEAIATVDRAINSTRTHLFDSRPRSPNDLLALFRYPRDPYTVEQA  673
Qy  749 PAGRTFDGDLARVSVEVIRDIRVK------NRVVFSGNCTNLSEAARAR           791
Db  674 RAGEIFERTLQLIQEHVQHGLMVDLNGTSYHYNDLVSPQYLNLIANLSGCT------AHRR 728
Qy  792 LVGLASAYQRQEKRV------DMLHGALGFLLKQFHGLL------PPRGMPPN---    832
Db  729 VNNCSDMCFHQKYRTHDGTCNNLQHPMWGASLTAFERLLKSVYENGFNTPRGINPHRLYN 788
Qy  833 ------SKSPNPQWFWTLLQRNQMPADKLTHEBITTIAAVK--RFTEE            872
Db  789 GHALPMPRLVSTTLLIGTETVTPDEQFTHMLMQWGQF---LDHDLDSTVVALSQARFSDG 844
Qy  873 YAAINFINLPPTCI------GELAQFYMANLILKYCDHSQYLINTLTSIITGA       919
Db  845 QHCSNVCSNDPPCFSVMIPNDSRARSGARCMFVRS------SPVCGSGMTSLLMNS    896
Qy  920 RRPRDPSSVLHWIRKDVTSAADIETQAKALLEKTENLPELWTTAFTSTH--LVRAAMNQR 977
Db  897 VYPREQINQL------TSYIDASNVYGSTEHEARSIRDL------ASHRGLLRQGIVQR  943
Qy  978 PMVVLGISISKYHGAAGNNRVFQAGNWSGLNGGKNVCPLFTFDRTRRFIIACPR----GG 1033
Db  944 ------SGKPLLFPATGPPTE------CMRDENESP                        967
Qy 1034 FICPVTGPSSGNRETTLSDQ----VRGIIVSGGAMVQL------AIYATVVRAVGARAQ 1082
Db  968 IPCFLAGDHRANEQLGLTSWHTLWFREHNRIATELLKLNPHWDGDTIYYETRKIVGAEIQ 1027
Qy 1083 HMAFPDDWLSLTDDEFIARDLEELH                                   1106
Db 1028 HITYQHWLPKILGEVGMRTLGEYH                                    1051
```

RESULT 32
US-10-211-462-87
; Sequence 87, Application US/10211462
; Publication No. US20040003495A1
APPLICANT: Murray, Richard
APPLICANT: Glynne, Richard
APPLICANT: Watson, Susan R.
APPLICANT: Aziz, Natasha
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Angiogenesis, Compositions and
TITLE OF INVENTION: Methods of screening for Angiogenesis Modulators
SEQ ID NO 87
; LENGTH: 1496
; TYPE: PRT

```
Db   961  -----------------SGKPLLPFATGPPTE-----CMRDENESP 984
Qy  1034  FICPVTGPSSGNRETTLSDQ----VRGIIVSGGAMVQL------AIYATVRVAVGARAQ 1082
Db   985  IPCFLAGDHRANEQLGLTSMHTLWFREHNRIATELLKLNPHWDGDTIYYETRKIVGAEIQ 1044
Qy  1083  HMAFDDWLSLTDDEFLARDLEELH 1106
Db  1045  HITYQHWLPKILGEVGMRTLGEYH 1068
```

RESULT 33
US-10-021-660-125
; Sequence 125, Application US/10021660
; Publication No. US2003015292 6A1
; GENERAL INFORMATION:
; APPLICANT: Murray, Richard
; APPLICANT: Glynne, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: EOS Biotechnology, Inc.
; TITLE OF INVENTION: No. US20030152926A1el Methods of Diagnosis of Angiogenesis,
; TITLE OF INVENTION: Compositions and Methods of Screening for Angiogenesis
; TITLE OF INVENTION: Modulators
; FILE REFERENCE: 018501-0007 10US
; CURRENT APPLICATION NUMBER: US/10/021,660
; CURRENT FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US/09/784,356
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/637,977
; PRIOR FILING DATE: 2000-08-11
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 125
; LENGTH: 1496
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-021-660-125

Query Match   1.8%;   Score 114.5;   DB 14;   Length 1496;
Best Local Similarity 18.5%;   Pred. No. 0.99;
Matches 204; Conservative 118; Mismatches 441; Indels 341; Gaps 47;

```
Qy   162  FKEAVFMCNVFLHYCGLDIVHINHGDVIRIPLFPVQLFMPD--VNRLVPDPFNTHHRSIG 219
Db   147  FKGLASLEQLYLHFNQIET--LDPDSFQHLPKLE-RLFLHNNRITTHLVPGTFN-HLESMK 202
Qy   220  EGFVYPTPFYNTGLCHLIHDCVIAPMAVALRVRNVTAVARGAAHLAPDENHBGAVLPPDI 279
Db   203  RLRLDS-----NTLHC----DCEIIWLADLLKTYABSGNAQAAAICEYPRR---------- 244
Qy   280  TYTYFQSSSSGTTARGARRNDVNSTSKFSPSGGFERRLASIMAADTALHAEVIFNTGIY 339
Db   245  ----IQGRSVATITPEELNCERPRITSEPQ---------------DADVTSGNTVY 281
Qy   340  BETPTDIKEWPMFIGMEG-------TLPRLNAL----------------GSYTARVAGVIG 377
Db   282  FTCRABGNPKPEIIWLRNNNELSMKTDSRLNLLDDGTLMIQNTQETDQGIYQCMAKNVAG 341
Qy   378  AMVFSPNSALYLTEVBDSGWTEAKDGGPGPSFNRFYQFAGPHLAANPQTDR---DGHVL 433
Db   342  -------------EVKTQEVTLRYFGSP--------ARPTFVIQPQNTEVLVGESVTL 378
Qy   434  SSQSTG---------SSNTEFSVDYIALICGFGAPLLARLLFYLERCDAGAFTGGHGDA 483
Db   379  ECSATGHPPPRISWTRGDRTPLPVDPRVNITPSGG-------LYIQ----NVVQGDSGEY 427
Qy   484  LKYVTGTFPDSEIPCSLCEKHTRPVCAHTTVHRLRQEMPRFGQATRQPIGVFG-TMNSQYS 542
Db   428  ACSATNNIDS----------VHATAFIIVQALPQFTVTPQDRVVIEGQTVDFQ-- 470
Qy   543  DCDPLGNYAPYLILRKPGDQTEAAAKATMQDTYRATLERLFIDLEQBRLLDRGA-PCSSEG 601
Db   471  -CEAKGNPPVIAWTKGGSQLSV------DRRHLVLSSGTLRISGVALHDQGQYECQAVN 523
```

```
Db   602  L--SSVIVDHPTFRRILDTLRARIEQTTQFMKVLVETRDYKIREGLSEATHSMALTFDP 659
Qy   524  IIGSQKVVAHLTVQPRVTPVFASIPSDTT----VEVGANVQLPCSSQGEPPAITWNK 577
Db   660  YSGAFCPITNFLVKRTHLAVVQDLA---LSQCHCVFYGQVEGRNF-RNQFQPVLRRRF 714
Qy   578  DGVQVTESGKFHiSPEGFLTINDVGPADAGRYECV-----ARNTIGSASVSMVLSVNV 630
Db   715  VDLFNGG--FIST-------RSITVT--LSEGPVSAPNPTLG------------QDA 748
Qy   631  PDVSRNGDPFVATSIVEAIATVDRAINSTRTHLFDSRPRSPNDLLALFRYPRDPYTVEQA 690
Db   749  PAGRTFDGDLARVSVEVIRDIRVK-----------NRVVFSGNCTNLSEAARAR 791
Qy   691  RAGEIFERTLQLIQEHVQHGLMVDLNGTSYHYNDLVSPQYLNLIANLSGCT-----AHRR 745
Db   792  LVGLASAYQRQEKRV------DMLHGALGFLLKQPHGLL----------FPRGMPPN---- 832
Qy   746  VNNCSDMCFHQKYRTHDGTCNNLQHPMWGASLTAFERLLKSVYENGFNTPRGINPHRLYN 805
Db   833  ----------------SKSPNPQWFWTLLQRNQMPADKLTHEBITTIAAVK--RFTEE 872
Qy   806  GHALPMPRLVSTTLIGTETVTPDEQFTHMLMQWGQF--LDHDLDSTVVALSQARFSDG 861
Db   873  YAAINFINLPPTCI----------GELAQFYMANLILKYCDHSQYLINTLTSIITGA 919
Qy   862  QHCSNVCSNDPPCFSVMIPPNDSRARSGARCMFVRS------SPVCGSGMTSLLMNS 913
Db   920  RRPRDPSSVLHWIRKDVTSAADIETQAKALLEKTENLPELWTTAFTSTH--LVRAAMNQR 977
Qy   914  VYPREQINQL------TSYIDASNVYGSTEHEARSIRDL------ASHRGLLRQGIVQR 960
Db   978  PMVVLGISISKYHGAAGNNRVFQAGNWSGLNGGKNVCPLFTFDRTRRFIIACPR----GG 1033
Qy   961  -----------------SGKPLLPFATGPPTE-----CMRDENESP 984
Db  1034  FICPVTGPSSGNRETTLSDQ----VRGIIVSGGAMVQL------AIYATVRVAVGARAQ 1082
Qy   985  IPCFLAGDHRANEQLGLTSMHTLWFREHNRIATELLKLNPHWDGDTIYYETRKIVGAEIQ 1044
Db  1083  HMAFDDWLSLTDDEFLARDLEELH 1106
Qy  1045  HITYQHWLPKILGEVGMRTLGEYH 1068
```

RESULT 34
US-10-331-496A-28
; Sequence 28, Application US/10331496A
; Publication No. US2003022830 5A1
; GENERAL INFORMATION:
; APPLICANT: FRANTZ, GRETCHEN
; APPLICANT: HILLAN, KENNETH J.
; APPLICANT: PHILLIPS, HEIDI S.
; APPLICANT: POLAKIS, PAUL
; APPLICANT: SMITH, VICTORIA
; APPLICANT: SPENCER, SUSAN D.
; APPLICANT: WILLIAMS, P. MICKEY
; APPLICANT: WU, THOMAS D.
; APPLICANT: ZHANG, ZEMIN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P5014R1-PCT
; CURRENT APPLICATION NUMBER: US/10/331,496A
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 60/345,444
; PRIOR FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: US 60/351,885
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: US 60/360,066
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: US 60/362,004
; PRIOR FILING DATE: 2002-03-05

```
; PRIOR APPLICATION NUMBER: US 60/366,869
; PRIOR FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: US 60/366,284
; PRIOR FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: US 60/368,679
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/404,809
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/405,645
; PRIOR FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 95
; SEQ ID NO 28
; LENGTH: 1496
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-331-496A-28

Query Match             1.8%;     Score 114.5; DB 15;  Length 1496;
Best Local Similarity   18.5%;    Pred. No. 0.99;
Matches   204;  Conservative 118; Mismatches 441; Indels 341; Gaps   47;

Qy     162  FKEAVFMCNVFLHYGGLDIVHINHGDVIRIPLFPVQLFMPD--VNRLVPDFPNTHHRSIG 219

Db     147  FKGLASLEQLYLHFNQIET--LDPDSFQHLPKLE-RLFLHNNRITHLVPGTFN-HLESMK 202

Qy     220  EGFVYPTPFYNTGLCHLIHDCVIAPMAVALRVRNVTAVARGAAHLAFDENHEGAVLPPDI 279

Db     244  RLRLDS-----NTLHC----DCEILWLADLLKTYAESGNAQAAAICEYPRR--------- 244

Qy     280  TYTYFQSSSGTTARGARRNDVNSTSKPSPSGGFERRLASIMAADTALHAEVIFNTGIY 339

Db     245  ---IQGRSVATITPELNCERPRITSEPQ----------------DADVTSGNTVY 281

Qy     340  EETPTDIKEWPMFIGMEG--------TLPRLNAL-------------GSYTARVAGVIG 377

Db     282  FTCRAEGNPKPEIIWLRNNELSMKTDSRLNLLDDGTLMIQNTQETDQGIYQCMAKNVAG 341

Qy     378  AMVFSPNSALYLTEVEDSGMTEAKDGGPGPSFNRFYQFAGPHLAANPQTDR----DGHVL 433

Db     342  ---------------EVKTQEVTLRYFGSP---------ARPTFVIQPQNTEVLVGESVTL 378

Qy     434  SSQSTG--------SSNTEFSVDYLALICGFGAPLLARLLFYLERCDAGAFTGGHGDA 483

Db     379  ECSATGHPPPRISWTRGDRTPLPVDPRVNIIPSGG-------LYIQ----NVVQGDSGEY 427

Qy     484  LKYVTGTFDSEIPCSLCEKHTRPVCAHTTVHRLRQRMPRFGQATRQPIGVFG-TVNSQYS 542

Db     428  ACSATNNIDS--------------VHATAFIIVQALPQFTVTPQDRVVIEGQTVDFQ-- 470

Db     543  DCDPLGNYAPYLILRKPGDQTEAAKATMQDTYRATLERLFIDLEQERLLDRGA-PCSSEG 601

Qy     471  -CEAKGNPPPVIAWTKGGSQLSV------DRRHLVLSSGTLRISGVALHDGQYECQAVN 523

Qy     602  L--SSIVDHPTFRRIIDTLRARIEQTTQFMKVLVETRDYKIREGLSEATHSMALTFDP 659

Db     524  IIGSQKVVAHLTVQPRVTPVFASIPSDTT-----VEVGANVQLPCSSQGEPEPAITWNK 577

Qy     660  YSGAFCPITNFLVKRTHLAVVCDLA--LSQCHCVFVGGQVEGRNF--RNQFQPVLRRRF 714

Db     578  DGVQVTESGKFHISPEGFLTINDVGPADAGRYECV------ARNTIGSASVSMVLSVNV 630

Qy     715  VDLFNGG--FIST--------RSIVT---LSEGPVSAPNPTLG---------QDA 748

Db     631  PDVSRNGDPFVATSIVEAIATVDRAINSTRTHLFDSRPRSPNDLLALFRYPRDPYTVEQA 690

Qy     749  PAGRTFDGDLARVSVEVIRDIRVK-------------NRVVFSGNCTNLSEAARAR 791

Db     691  RAGEIFERTLQLIQEHVQHGLMVDLNGTSYHYNDLVSPQYLNLIANLSGCT-----AHRR 745

Qy     792  LVGLASAYQRQERKV------DMLHGALGFLLKQFHGLL--------FPRGMPPN----- 832

Db     746  VNNCSDMCFHQKYRTHDGTCNNLQHPWMGASLTAFERLLKSVYENGFNTPRGINPHRLYN 805
```

```
Qy     833  ----------------SKSPNPQWFWTLLQRNQMPADKLTHEEITTIAAVK--RFTEE 872

Db     806  GHALPMPRLVSTTLIGTETVIPDEQFTHMLMQWGQF---LDHDLDSTVVALSQARFSDG 861

Qy     873  YAAINFINLPPTCI------------GELAQFYMANLILKYCDHSQYLINTLTSIITGA 919

Db     862  QHCSNVCSNDPPCFSVMIPPNDSRARSGARCMFFVRS----SPVCGSGMTSLLMNS 913

Qy     920  RRPRDPSSVLHWIRKDVTSAADIETQAKALLEKTENLPELWTTAFTSTH--IVRAAMNQR 977

Db     914  VYPREQINQL-------TSYIDASNVYGSTEHEARSIRDL------ASHRGLLRQGIVQR 960

Qy     978  PMVVLGISISKYHGAAGNNRVFQAGNWSGLNGGKNVCPLFTFDRTRRFIIACPR----GG 1033

Db     961  -------------------------SGKPLLPFATGPPTE-----CMRDENESP 984

Qy    1034  FICPVTGPSSGNRETTLSDQ---VRGIIVSGGAMVQL------AIYATVRAVGARAQ 1082

Db     985  IPCFLAGDHRANEQLGLTSMHTLMFREHNRIATELLKLNPHWDGDTIYETRKIVGAEIQ 1044

Qy    1083  HMAFDDWLSLTDEFLADLEELH 1106

Db    1045  HITYQHWLPKILGEVGMRTLGEYH 1068
```

```
RESULT 35
US-10-276-774-1957
; Sequence 1957, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang, Y, Tom et al
; TITLE OF INVENTION: No. US20040005324SA1e1 Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 1957
; LENGTH: 1498
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-276-774-1957

Query Match             1.8%;     Score 114.5; DB 12;  Length 1498;
Best Local Similarity   18.5%;    Pred. No. 0.99;
Matches   204;  Conservative 118; Mismatches 441; Indels 341; Gaps   47;

Qy     162  FKEAVFMCNVFLHYGGLDIVHINHGDVIRIPLFPVQLFMPD--VNRLVPDFPNTHHRSIG 219

Db     147  FKGLASLEQLYLHFNQIET--LDPDSFQHLPKLE-RLFLHNNRITHLVPGTFN-HLESMK 202

Qy     220  EGFVYPTPFYNTGLCHLIHDCVIAPMAVALRVRNVTAVARGAAHLAFDENHEGAVLPPDI 279

Db     203  RLRLDS-----NTLHC----DCEILWLADLLKTYAESGNAQAAAICEYPRR--------- 244

Qy     280  TYTYFQSSSGTTARGARRNDVNSTSKPSPSGGFERRLASIMAADTALHAEVIFNTGIY 339

Db     245  ----IQGRSVATITPELNCERPRITSEPQ----------------DADVTSGNTVY 281

Qy     340  EETPTDIKEWPMFIGMEG--------TLPRLNAL-------------GSYTARVAGVIG 377

Db     282  FTCRAEGNPKPEIIWLRNNELSMKTDSRLNLLDDGTLMIQNTQETDQGIYQCMAKNVAG 341

Qy     378  AMVFSPNSALYLTEVEDSGMTEAKDGGPGPSFNRFYQFAGPHLAANPQTDR----DGHVL 433

Db     342  ---------------EVKTQEVTLRYFGSP---------ARPTFVIQPQNTEVLVGESVTL 378

Qy     434  SSQSTG--------SSNTEFSVDYLALICGFGAPLLARLLFYLERCDAGAFTGGHGDA 483
```

Thu Jun 3 08:06:33 2004   us-09-769-699-2.rapb

```
Db   379  ECSATGHPPPRISWTRGDRTPLFVDPRVNITPSGG--------LYIQ---NVVQGDSGEY  427
              ||    :    :                              |::
Qy   484  LKVVTGTFDSEIPCSLCEKHTRPVCAHTVHRLRQRMPRFGQATRQPIGVFG-TMNSQYS  542
              |         : :  ::                |  : :  |::
Db   428  ACSATNNIDS-----------VHATAFIIVQALPQFTVTPQDRVVIEGQTVDFQ--  470

Qy   543  DCDPLGNYAPYLILRKPGDQTEAAKATMQDTYRATLERLFIDLEQERLLDRGA-PCSSEG  601
              |:  ||   :          |||   || ||||  :|:  |::
Db   471  -CEAKGNPPPVIAWTKGGSQLSV-----DRRHIVLSSGTLRISGVALHDQGQYECQAVN  523

Qy   602  L--SSVIVDHPTFRRILDTLRARIEQTTTQFMKVLVETRDYKIREGLSEATHSMALTFDP  659
              :   ||    |:|  : ||                 || ||  |:|:|
Db   524  IIGSQKVVAHLTVQPRVTPVFASIPSDTT------VEVGANVQLPCSSQGEPEPAITWNK  577

Qy   660  YSGAFCPITNFLVKRTHLAVVQDLA---LSQCHVFYGQQVEGRNF--RNQFQPVLRRRF  714
              |  : :  :  ::  :      :           :  ||
Db   578  DGVQVTESGKFHISPEGFLTINDVGPADAGRYECV------ARNTIGSASVSMVLSVNV  630

Qy   715  VDLFNGG--FIST--------RSITVT----LSEGPVSAPNPTLG---------QDA  748
              |   :  |::  : :        : :              :
Db   631  PDVSRNGDPFVATSIVEAIATVDRAINSTRTHLFDSRPRSPNDLLALFRYPRDPYTVEQA  690

Qy   749  PAGRTFDGDLARVSVEVIRDIRVK---------NRVVFSGNCTNLSEAARAR  791
              |  :     |:    ||                   |:|
Db   691  RAGEIFERTLQLIQEHVQHGLMVDLNGTSYHYNDLVSPQYLNLIANLSGCT----AHRR  745

Qy   792  LVGLASAYQRQEKRV------DMLHGALGFLLKQFHGLL--------FPRGMPPN---  832
              :|  :  :           |: |  |  : |  |         ||: |:
Db   746  VNNCSDMCFHQKYRTHDGTCNNLQHPMWGASLTAFERLLKSVYENGFNTPRGINPHRLYN  805

Qy   833  ----------SKSPNPQWFWTLLQRNQMPADKLTHEITTIAAVK--RFTEE  872
              :  : |:  | : :  : |  :     :| :: :: |  | :: |
Db   806  GHALPMPRLVSTTLIGTETVTPDEQFTHMLMQWGQF----LDHDLDSTVVALSQARFSDG  861

Qy   873  YAAINFINLPTCI----------GELAQFYMANLILKYCDHSQYLINTLTSIITGA  919
              |  : :  |  :               : :  :   : :::|
Db   862  QHCSNVCSNDPPCFSVMIPPNDSRARSGARCMFFVRS--------SPVCCSGMTSLLMNS  913

Qy   920  RRPRDPSSVLHWIRKDVTSAADIETQAKALLEKTENLPELWTTAFTSTH--LVRAAMNQR  977
              :  ||     : :      : |::: : ::       |  :    |:
Db   914  VYPREQINQL-------TSYIDASNVYGSTHEARSIRDL------ASHRGLLRQGIVQR  960

Qy   978  PMVVLGISISKYHGAAGNNRVFQAGNWSGLNGGKNVCPLFTFDRTRRFIIACPR-----GG  1033
              :   ::   |                                   :
Db   961  ----------------------SGKPLLPFATGPPTE-----CMRDENESP  984

Qy   1034 FICPVTGPSSGNRETTLSDQ---VRGIIVSGGAMVQL------AIYATVVRAVGARAQ  1082
              |:            :::                         |||
Db   985  IPCFLAGDHRANEQLGLTSMHTLWFREHNRIATELLKLNPHWDGDTIYYETRKIVGABIQ  1044

Qy   1083 HMAFDDWLSLTDDEFLARDLEELH  1106
              |::
Db   1045 HITYQHWLPKIIGEVGMRTLGEYH  1068
```

Search completed: June 3, 2004, 07:14:06
Job time : 562 secs